

Figure 1: 158P1D7 SSH sequence (SEQ ID NO:1) .

```
1  GATCTGATAA  GCTTTCAATG  TTGCGCTCCT  GACAATGTAT  TAGAAGTCCT  GATGGGGATA
61 GGACTTTGCA  GTTACAAGGA  ATAGGGCAGA  AAGGTCCTGG  AAGTTGAGTG  GATGGCTTTG
121 TAATATAAGG  TATCAAACCT  GGTGCTTTGG  TGGGTAGTTT  TAGAATGGAC  GTGGTCTTAG
181 TTGACATGCG  ACTATCATTT  ATTGAAGATG  TTGCTGCCAG  ATGTAATGAT  C
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Figure 2:**Figure 2A-1. The cDNA (SEQ ID NO:2) and amino acid sequence (SEQ ID NO:3) of 158P1D7 v.1.**

The start methionine is underlined. The open reading frame extends from nucleic acid 23-2548 including the stop codon.

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1           M K L W I H L F Y S S L L
1  tcggatttcatcacatgacaacATGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCT
14  A C I S L H S Q T P V L S S R G S C D S
61  TGCCTGTATATCTTTACACTCCCCAACTCCAGTGCTCTCATCCAGAGGCTCTTGTGATTC
34  L C N C E E K D G T M L I N C E A K G I
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAGGTAT
54  K M V S E I S V P P S R P F Q L S L L N
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAACTAAGCTTATTA
74  N G L T M L H T N D F S G L T N A I S I
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT
94  H L G F N N I A D I E I G A F N G L G L
301 ACACCTTGGATTTAACAATATTGCAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCT
114 L K Q L H I N H N S L E I L K E D T F H
361 CCTGAAACAACCTTCATATCAATCACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCA
134 G L E N L E F L Q A D N N F I T V I E P
421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
154 S A F S K L N R L K V L I L N D N A I E
481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
174 S L P P N I F R F V P L T H L D L R G N
541 GAGTCTTCCTCCAAACATCTTCCGATTTGTTCTTTAACCCATCTAGATCTTCGTGGAAA
194 Q L Q T L P Y V G F L E H I G R I L D L
601 TCAATTACAAACATTGCCTTATGTTGGTTTTCTCGAACACATTGGCCGAATATTGGATCT
214 Q L E D N K W A C N C D L L Q L K T W L
661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT
234 E N M P P Q S I I G D V V C N S P P F F
721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTT
254 K G S I L S R L K K E S I C P T P P V Y
781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
274 E E H E D P S G S L H L A A T S S I N D
841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
294 S R M S T K T T S I L K L P T K A P G L
901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACTACCCACCAAAGCACCAGGTTT
314 I P Y I T K P S T Q L P G P Y C P I P C
961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTCTCTG
334 N C K V L S P S G L L I H C Q E R N I E

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Figure 2A-2

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1021 TAACTGCAAAGTCCTATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA
354 S L S D L R P P P Q N P R K L I L A G N
1081 AAGCTTATCAGATCTGAGACCTCCTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGGAAA
374 I I H S L M K S D L V E Y F T L E M L H
1141 TATTATTCACAGTTTAAATGAAGTCTGATCTAGTGGAATATTTCACTTTGGAAATGCTTCA
394 L G N N R I E V L E E G S F M N L T R L
1201 CTTGGGAAACAATCGTATTGAAGTTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATT
414 Q K L Y L N G N H L T K L S K G M F L G
1261 ACAAAAACCTCTATCTAAATGGTAACCACTGACCAAATTAAGTAAAGGCATGTTCTTGG
434 L H N L E Y L Y L E Y N A I K E I L F G
1321 TCTCCATAATCTTGAATACTTATATCTTGAATACAATGCCATTAAGGAAATACTGCCAGG
454 T F N P M P K L K V L Y L N N N L L Q V
1381 AACCTTTAATCCAATGCCTAAACTTAAAGTCCTGTATTTAAATAACAACCTCCTCCAAGT
474 L P P H I F S G V P L T K V N L K T N Q
1441 TTTACCACCACATATTTTTTTCAGGGGTTCTCTAACTAAGGTAAATCTTAAAACAAACCA
494 F T H L P V S N I L D D L D L L T Q I D
1501 GTTTACCCATCTACCTGTAAGTAATATTTTGGATGATCTTGATTTACTAACCCAGATTGA
514 L E D N P W D C S C D L V G L Q Q W I Q
1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTGGACTGCAGCAATGGATACA
534 K L S K N T V T D D I L C T S P G H L D
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACTTCCCCCGGGCATCTCGA
554 K K E L K A L N S E I L C P G L V N N P
1681 CAAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC
574 S M P T Q T S Y L M V T T P A T T T N T
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAAATAC
594 A D T I L R S L T D A V P L S V L I L G
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG
614 L L I M F I T I V F C A A G I V V L V L
1861 ACTTCTGATTATGTTTCATCACTATTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTCT
634 H R R R R Y K K K Q V D E Q M R D N S P
1921 TCACCGCAGGAGAAGATACAAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC
654 V H L Q Y S M Y G H K T T H H T T E R P
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCACACTACTGAAAGACC
674 S A S L Y E Q H M V S P M V H V Y R S P
2041 CTCTGCCTCACTCTATGAACAGCACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCC
694 S F G P K H L E E E E E R N E K E G S D
2101 ATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGA
714 A K H L Q R S L L E Q E N H S P L T G S
2161 TGCAAAACATCTCCAAAGAAGTCTTTTGGAACAGGAAAATCATTCACTACTCACAGGGTC
734 N M K Y K T T N Q S T E F L S F Q D A S

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Figure 2A-3

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2221 AAATATGAAATACAAAACACGAACCAATCAACAGAATTTTTATCCTTCCAAGATGCCAG
754  S L Y R N I L E K E R E L Q Q L G I T E
2281 CTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGAACCTCAGCAACTGGGAATCACAGA
774  Y L R K N I A Q L Q P D M E A H Y P G A
2341 ATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGATATGGAGGCACATTATCCTGGAGC
794  H E E L K L M E T L M Y S R P R K V L V
2401 CCACGAAGAGCTGAAGTTAATGGAAACATTAATGTACTCACGTCCAAGGAAGGTATTAGT
814  E Q T K N E Y F E L K A N L H A E P D Y
2461 GGAACAGACAAAAAATGAGTATTTTGAACCTAAAGCTAATTTACATGCTGAACCTGACTA
834  L E V L E Q Q T *
2521 TTTAGAAGTCCTGGAGCAGCAACATAGatggaga

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Figure 2B-1. The cDNA (SEQ ID NO:4) and amino acid sequence (SEQ ID NO:5) of 158P1D7 v.2.

The start methionine is underlined. The open reading frame extends from nucleic acid 23-2548 including the stop codon.

```

1           M K L W I H L F Y S S L L
1  tcggatttcatcacatgacaacATGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCT
14  A C I S L H S Q T P V L S S R G S C D S
61  TGCCTGTATATCTTTTACTTCCAACTCCAGTGCTCTCATCCAGAGGCTCTTGTGATTC
34  L C N C E E K D G T M L I N C E A K G I
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAGGTAT
54  K M V S E I S V P P S R P F Q L S L L N
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAATAAGCTTATTAAA
74  N G L T M L H T N D F S G L T N A I S I
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT
94  H L G F N N I A D I E I G A F N G L G L
301 ACACCTTGGATTTAACAATATTGCAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCT
114 L K Q L H I N H N S L E I L K E D T F H
361 CCTGAAACAACTTCATATCAATCACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCA
134 G L E N L E F L Q A D N N F I T V I E P
421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
154 S A F S K L N R L K V L I L N D N A I E
481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
174 S L P P N I F R F V P L T H L D L R G N
541 GAGTCTTCCTCCAAACATCTTCCGATTTGTTCCCTTTAACCCATCTAGATCTTCGTGGAAA
194 Q L Q T L P Y V G F L E H I G R I L D L
601 TCAATTACAAACATTGCCTTATGTTGGTTTTCTCGAACACATTGGCCGAATATTGGATCT
214 Q L E D N K W A C N C D L L Q L K T W L
661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT

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Figure 2B-2

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234 E N M P P Q S I I G D V V C N S P P F F
721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTTT
254 K G S I L S R L K K E S I C P T P P V Y
781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
274 E E H E D P S G S L H L A A T S S I N D
841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
294 S R M S T K T T S I L K L P T K A P G L
901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACCTACCCACCAAAGCACCAGGTTT
314 I P Y I T K P S T Q L P G P Y C P I P C
961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTTCCTTG
334 N C K V L S P S G L L I H C Q E R N I E
1021 TAACTGCAAAGTCCTATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA
354 S L S D L R F P P Q N P R K L I L A G N
1081 AAGCTTATCAGATCTGAGACCTCCTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGGAAA
374 I I H S L M K S D L V E Y F T L E M L H
1141 TATTATTACAGTTTAAATGAAGTCTGATCTAGTGGAATATTTCACTTTGGAAATGCTTCA
394 L G N N R I E V L E E G S F M N L T R L
1201 CTTGGGAAACAATCGTATTGAAGTTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATT
414 Q K L Y L N G N H L T K L S K G M F L G
1261 ACAAAAACCTCTATCTAAATGGTAACCACCTGACCAAATTAAGTAAAGGCATGTTCCCTTGG
434 L H N L E Y L Y L E Y N A I K E I L P G
1321 TCTCCATAATCTTGAATACTTATATCTTGAATACAATGCCATTAAGGAAATACTGCCAGG
454 T F N P M P K L K V L Y L N N N L L Q V
1381 AACCTTTAATCCAATGCCTAAACTTAAAGTCCTGTATTTAAATAACAACCTCCTCCAAGT
474 L P P H I F S G V P L T K V N L K T N Q
1441 TTTACCACCACATATTTTTTTCAGGGGTTCCCTCTAACTAAGGTAAATCTTAAAACAAACCA
494 F T H L P V S N I L D D L D L L T Q I D
1501 GTTTACCCATCTACCTGTAAGTAATATTTTGGATGATCTTGATTTGCTAACCCAGATTGA
514 L E D N P W D C S C D L V G L Q Q W I Q
1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACA
534 K L S K N T V T D D I L C T S P G H L D
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACTTCCCCCGGCATCTCGA
554 K K E L K A L N S E I L C P G L V N N P
1681 CAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC
574 S M P T Q T S Y L M V T T P A T T T N T
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAAATAC
594 A D T I L R S L T D A V P L S V L I L G
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG
614 L L I M F I T I V F C A A G I V V L V L
1861 ACTTCTGATTATGTTTCATCACTATTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTCT

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Figure 2B-3

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634  H R R R R Y K K K Q V D E Q M R D N S P
1921 TCACCGCAGGAGAAGATACAAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC
654  V H L Q Y S M Y G H K T T H H T T E R P
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCACACTACTGAAAGACC
674  S A S L Y E Q H M V S P M V H V Y R S P
2041 CTCTGCCTCACTCTATGAACAGCACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCC
694  S F G P K H L E E E E E R N E K E G S D
2101 ATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGA
714  A K H L Q R S L L E Q E N H S P L T G S
2161 TGCAAAACATCTCCAAAGAAGTCTTTTGGAAACAGGAAAATCATTCCACCACTCACAGGGTC
734  N M K Y K T T N Q S T E F L S F Q D A S
2221 AAATATGAAATACAAAACCACGAACCAATCAACAGAATTTTTATCCTTCCAAGATGCCAG
754  S L Y R N I L E K E R E L Q Q L G I T E
2281 CTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGAAGTTCAGCAACTGGGAATCACAGA
774  Y L R K N I A Q L Q P D M E A H Y P G A
2341 ATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGATATGGAGGCACATTATCCTGGAGC
794  H E E L K L M E T L M Y S R P R K V L V
2401 CCACGAAGAGCTGAAGTTAATGGAAACATTAATGTACTCACGTCCAAGGAAGGTATTAGT
814  E Q T K N E Y F E L K A N L H A E P D Y
2461 GGAACAGACAAAAAATGAGTATTTTGAAGCTTAAAGCTAATTTACATGCTGAACCTGACTA
834  L E V L E Q Q T *
2521 TTTAGAAGTCCTGGAGCAGCAAACATAGatggaga

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Figure 2C-1. The cDNA (SEQ ID NO:6) and amino acid sequence (SEQ ID NO:7) of 158P1D7 v.3.

The start methionine is underlined. The open reading frame extends from nucleic acid 23-2221 including the stop codon.

```

1          M K L W I H L F Y S S L L
1  tcggatttcatcacatgacaacATGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCT
14  A C I S L H S Q T P V L S S R G S C D S
61  TGCCTGTATATCTTTACACTCCCAAACCTCCAGTGCTCTCATCCAGAGGCTCTTGTGATTC
34  L C N C E E K D G T M L I N C E A K G I
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAAGGTAT
54  K M V S E I S V P P S R P F Q L S L L N
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAATAAGCTTATTTAAA
74  N G L T M L H T N D F S G L T N A I S I
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT
94  H L G F N N I A D I E I G A F N G L G L
301 ACACCTTGGATTAAACAATATTGCAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCT
114 L K Q L H I N H N S L E I L K E D T F H

```

Figure 2C-2

361 CCTGAAACAACCTTCATATCAATCACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCA
134 G L E N L E F L Q A D N N F I T V I E P
421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
154 S A F S K L N R L K V L I L N D N A I E
481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
174 S L P P N I F R F V P L T H L D L R G N
541 GAGTCTTCCTCCAAACATCTTCCGATTTGTTCTTTAACCCATCTAGATCTTCGTGGAAA
194 Q L Q T L P Y V G F L E H I G R I L D L
601 TCAATTACAAACATTGCCTTATGTTGGTTTTCTCGAACACATTGGCCGAATATTGGATCT
214 Q L E D N K W A C N C D L L Q L K T W L
661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT
234 E N M P P Q S I I G D V V C N S P P F F
721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTTT
254 K G S I L S R L K K E S I C P T P P V Y
781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
274 E E H E D P S G S L H L A A T S S I N D
841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
294 S R M S T K T T S I L K L P T K A P G L
901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACCTACCCACCAAAGCACCAGGTTT
314 I P Y I T K P S T Q L P G P Y C P I P C
961 GATACCTTATATTACAAAGCCATCCACTCAACTCCAGGACCTTACTGCCCTATTCCTTG
334 N C K V L S P S G L L I H C Q E R N I E
1021 TAACTGCAAAGTCCTATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA
354 S L S D L R P P P Q N P R K L I L A G N
1081 AAGCTTATCAGATCTGAGACCTCCTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGGAAA
374 I I H S L M K S D L V E Y F T L E M L H
1141 TATTATTCACAGTTTAAATGAAGTCTGATCTAGTGGAATATTTCACTTTGGAAATGCTTCA
394 L G N N R I E V L E E G S F M N L T R L
1201 CTTGGGAAACAATCGTATTGAAGTTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATT
414 Q K L Y L N G N H L T K L S K G M F L G
1261 ACAAAAACCTCTATCTAAATGGTAACCACCTGACCAAATTAAGTAAAGGCATGTTCTTGG
434 L H N L E Y L Y L E Y N A I K E I L P G
1321 TCTCCATAATCTTGAATACTTATATCTTGAATACAATGCCATTAAGGAAATACTGCCAGG
454 T F N P M P K L K V L Y L N N N L L Q V
1381 AACCTTTAATCCAATGCCTAAACTTAAAGTCCTGTATTTAAATAACAACCTCCTCCAAGT
474 L P P H I F S G V P L T K V N L K T N Q
1441 TTTACCACCACATATTTTTTTCAGGGGTTCTCTAACTAAGGTAAATCTTAAAACAAACCA
494 F T H L P V S N I L D D L D L L T Q I D
1501 GTTTACCCATCTACCTGTAAGTAATATTTTGGATGATCTTGATTTACTAACCCAGATTGA
514 L E D N P W D C S C D L V G L Q Q W I Q

Figure 2C-3

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1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACA
534 K L S K N T V T D D I L C T S P G H L D
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACTTCCCCGGGCATCTCGA
554 K K E L K A L N S E I L C P G L V N N P
1681 CAAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC
574 S M P T Q T S Y L M V T T P A T T T N T
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAAATAC
594 A D T I L R S L T D A V P L S V L I L G
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG
614 L L I M F I T I V F C A A G I V V L V L
1861 ACTTCTGATTATGTTTCATCACTATTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTTCT
634 H R R R R Y K K K Q V D E Q M R D N S P
1921 TCACCGCAGGAGAAGATACAAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC
654 V H L Q Y S M Y G H K T T H H T T E R P
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCACTACTGAAAGACC
674 S A S L Y E Q H M G A H E E L K L M E T
2041 CTCTGCCTCACTCTATGAACAGCACATGGGAGCCCACGAAGAGCTGAAGTTAATGGAAAC
694 L M Y S R P R K V L V E Q T K N E Y F E
2101 ATTAATGTACTCACGTCCAAGGAAGGTATTAGTGGAACAGACAAAAAATGAGTATTTTGA
714 L K A N L H A E P D Y L E V L E Q Q T *
2161 ACTTAAAGCTAATTTACATGCTGAACCTGACTATTTAGAAGTCCTGGAGCAGCAAACATA
2221 Gatggaga

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Figure 2D-1. The cDNA (SEQ ID NO:8) and amino acid sequence (SEQ ID NO:9) of 158P1D7 v.4.

The start methionine is underlined. The open reading frame extends from nucleic acid 23-1210 including the stop codon.

```

1 M K L W I H L F Y S S L L
1 tcggatttcatcacatgacaacATGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCT
14 A C I S L H S Q T P V L S S R G S C D S
61 TGCCTGTATATCTTTTACACTCCCAAACCTCCAGTGCTCTCATCCAGAGGCTCTTGATTC
34 L C N C E E K D G T M L I N C E A K G I
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAGGTAT
54 K M V S E I S V P P S R P F Q L S L L N
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAATAAGCTTATTAAA
74 N G L T M L H T N D F S G L T N A I S I
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT
94 H L G F N N I A D I E I G A F N G L G L
301 ACACCTTGGATTTAACAATATTGCAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCT
114 L K Q L H I N H N S L E I L K E D T F R

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Figure 2D-2

361 CCTGAAACAACCTTCATATCAATCACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCA
 134 G L E N L E F L Q A D N N F I T V I E P
 421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
 154 S A F S K L N R L K V L I L N D N A I E
 481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
 174 S L P P N I F R F V P L T H L D L R G N
 541 GAGTCTTCCTCCAAACATCTTCCGATTTGTTCCCTTAACCCATCTAGATCTTCGTGGAAA
 194 Q L Q T L P Y V G F L E H I G R I L D L
 601 TCAATTACAAACATTGCCTTATGTTGGTTTTCTCGAACACATTGGCCGAATATTGGATCT
 214 Q L E D N K W A C N C D L L Q L K T W L
 661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT
 234 E N M P P Q S I I G D V V C N S P P F F
 721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTTT
 254 K G S I L S R L K K E S I C P T P P V Y
 781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
 274 E E H E D P S G S L H L A A T S S I N D
 841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
 294 S R M S T K T T S I L K L P T K A P G L
 901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACCTACCCACCAAAGCACCAGGTTT
 314 I P Y I T K P S T Q L F G P Y C P I P C
 961 GATACCTTATATTACAAAGCCATCCACTCAACTCCAGGACCTTACTGCCCTATTCCTTG
 334 N C K V L S P S G L L I H C Q E R N I E
 1021 TAACTGCAAAGTCCTATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA
 354 S L S D L R P P P Q N P R K L I L A G N
 1081 AAGCTTATCAGATCTGAGACCTCCTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGGAAA
 374 I I H S L M K S I L W S K A S G R G R R
 1141 TATTATTCACAGTTTAATGAAGTCCATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAG
 394 E E *
 1201 AGAGGAATGAgaaagaaggaagtgatgcaaaacatctccaaagaagtcttttggaaacagg
 1261 aaaatcattcaccactcacaggggtcaaatatgaaatacaaaaccacgaaccaatcaacag
 1321 aatttttatccttccaagatgccagctcattgtacagaaacattttagaaaaagaaaggg
 1381 aacttcagcaactgggaatcacagaatacctaaggaaaaacattgctcagctccagcctg
 1441 atatggaggcacattatcctggagcccacgaagagctgaagttaatggaaacattaatgt
 1501 actcacgtccaaggaaggtatttagtggaaacagacaaaaaatgagtattttgaacttaaag
 1561 ctaatttacatgctgaacctgactatttagaagtcctggagcagcaaacatagatggaga

Figure 2E-1. The cDNA (SEQ ID NO:10) and amino acid sequence (SEQ ID NO:11) of 158P1D7 v.5.

The start methionine is underlined. The open reading frame extends from nucleic acid 480-3005 including the stop codon.

```
1 gcgtcgacaacaagaaatactagaaaaggaggaaggagaacattgctgcagcttggatct
61 acaacctaagaaagcaagagtgatcaatctcagctctgttaaacaatcttgtttacttact
121 gcattcagcagcttgcaaattgggttaactatatgcaaaaaagtcagcatagctgtgaagta
181 tgccgtgaatttttaattgagggaaaaaggacaattgcttcaggatgctctagtatgcact
241 ctgcttgaaatattttcaatgaaatgctcagttattctatctttgaccagagggttttaact
301 ttatgaagctatgggacttgacaaaaagtgatatttgagaagaaagtacgcagtggttg
361 tgttttcttttttttaataaaggaattgaattactttgaacacctcttccagctgtgcat
1 M
421 tacagataacgtcaggaagagtctctgctttacagaatcggatttcatcacatgacaacA
2 K L W I H L F Y S S L L A C I S L H S Q
481 TGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCTTGCCTGTATATCTTTACACTCCC
22 T P V L S S R G S C D S L C N C E E K D
541 AAACCTCCAGTGCTCTCATCCAGAGGCTCTTGTGATTCTCTTTGCAATTGTGAGGAAAAAG
42 G T M L I N C E A K G I K M V S E I S V
601 ATGGCACAATGCTAATAAATTGTGAAGCAAAAGGTATCAAGATGGTATCTGAAATAAGTG
62 P P S R P F Q L S L L N N G L T M L H T
661 TGCCACCATCACGACCTTTCCAATAAGCTTATTAATAACGGCTTGACGATGCTTCACA
82 N D F S G L T N A I S I H L G F N N I A
721 CAAATGACTTTTCTGGGCTTACCAATGCTATTTCAATACACCTTGGATTTAACAATATTG
102 D I E I G A F N G L G L L K Q L H I N H
781 CAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCTCCTGAAACAACTTCATATCAATC
122 N S L E I L K E D T F H G L E N L E F L
841 ACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCATGGACTGGAAAACCTGGAATTCC
142 Q A D N N F I T V I E P S A F S K L N R
901 TGCAAGCAGATAACAATTTTATCACAGTGATTGAACCAAGTGCCTTTAGCAAGCTCAACA
162 L K V L I L N D N A I E S L P P N I F R
961 GACTCAAAGTGTTAATTTTAAATGACAATGCTATTGAGAGTCTTCCTCCAAACATCTTCC
182 F V P L T H L D L R G N Q L Q T L P Y V
1021 GATTTGTTTCCTTTAACCCATCTAGATCTTCGTGGAAATCAATTACAAACATTGCCTTATG
202 G F L E H I G R I L D L Q L E D N K W A
1081 TTGGTTTTCTCGAACACATTGGCCGAATATTGGATCTTCAGTTGGAGGACAACAAATGGG
222 C N C D L L Q L K T W L E N M P P Q S I
1141 CCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTTGGAGAACATGCCTCCACAGTCTA
242 I G D V V C N S P P F F K G S I L S R L
1201 TAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTTTTAAAGGAAGTATACTCAGTAGAC
262 K K E S I C P T P P V Y E E H E D P S G
1261 TAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTATGAAGAACATGAGGATCCTTCAG
```

Figure 2E-2

282 S L H L A A T S S I N D S R M S T K T T
1321 GATCATTACATCTGGCAGCAACATCTTCAATAAATGATAGTCGCATGTCAACTAAGACCA
302 S I L K L P T K A P G L I P Y I T K P S
1381 CGTCCATTCTAAAACTACCCACCAAAGCACCAGGTTTGATACCTTATATTACAAAGCCAT
322 T Q L P G P Y C P I P C N C K V L S P S
1441 CCACTCAACTTCCAGGACCTTACTGCCCTATTCCTTGTAAGTCAAAGTCCTATCCCCAT
342 G L L I H C Q E R N I E S L S D L R P F
1501 CAGGACTTCTAATACATTGTCTCAGGAGCGCAACATTGAAAGCTTATCAGATCTGAGACCTC
362 P Q N P R K L I L A G N I I H S L M K S
1561 CTCCGCAAATCCTAGAAAGCTCATTCTAGCGGAAATATTATTACAGTTTAAATGAAGT
382 D L V E Y F T L E M L H L G N N R I E V
1621 CTGATCTAGTGGAATATTTCACTTTGGAAATGCTTCACTTGGGAAACAATCGTATTGAAG
402 L E E G S F M N L T R L Q K L Y L N G N
1681 TTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATTACAAAACCTCTATCTAAATGGTA
422 H L T K L S K G M F L G L H N L E Y L Y
1741 ACCACCTGACCAAATTAAGTAAAGGCATGTTCTTGGTCTCCATAATCTTGAATACTTAT
442 L E Y N A I K E I L P G T F N P M P K L
1801 ATCTTGAATACAATGCCATTAAGGAAATACTGCCAGGAACCTTTAATCCAATGCCTAAAC
462 K V L Y L N N N L L Q V L P P H I F S G
1861 TTAAAGTCCTGTATTTAAATAACAACCTCCTCCAAGTTTTACCACCACATATTTTTTTCAG
482 V P L T K V N L K T N Q F T H L P V S N
1921 GGGTTCCTCTAACTAAGGTAAATCTTAAAACAAACCAGTTTACCCATCTACCTGTAAAGTA
502 I L D D L D L L T Q I D L E D N P W D C
1981 ATATTTTGGATGATCTTGATTTACTAACCCAGATTGACCTTGAGGATAACCCCTGGGACT
522 S C D L V G L Q Q W I Q K L S K N T V T
2041 GCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACAAAAGTTAAGCAAGAACACAGTGA
542 D D I L C T S P G H L D K K E L K A L N
2101 CAGATGACATCCTCTGCACTTCCCCCGGCATCTCGACAAAAGGAATTGAAAGCCCTAA
562 S E I L C P G L V N N P S M P T Q T S Y
2161 ATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCCATCCATGCCAACACAGACTAGTT
582 L M V T T P A T T T N T A D T I L R S L
2221 ACCTTATGGTCACCACTCCTGCAACAACAACAAATACGGCTGATACTATTTTACGATCTC
602 T D A V P L S V L I L G L L I M F I T I
2281 TTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGGACTTCTGATTATGTTCACTACTA
622 V F C A A G I V V L V L H R R R R Y K K
2341 TTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTCTTCACCGCAGGAGAAGATACAAAA
642 K Q V D E Q M R D N S P V H L Q Y S M Y
2401 AGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCCTGTGCATCTTCAGTACAGCATGT
662 G H K T T H H T T E R P S A S L Y E Q H
2461 ATGGCCATAAAACCACTCATCACACTACTGAAAGACCCTCTGCCTCACTCTATGAACAGC

Figure 2E-3

```

682   M V S P M V H V Y R S P S F G P K H L E
2521 ACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCCATCCTTTGGTCCAAAGCATCTGG
702   E E E E R N E K E G S D A K H L Q R S L
2581 AAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGATGCAAAACATCTCCAAAGAAGTC
722   L E Q E N H S P L T G S N M K Y K T T N
2641 TTTTGGAACAGGAAAATCATTCACTACTCACAGGGTCAAATATGAAATACAAAACCACGA
742   Q S T E F L S F Q D A S S L Y R N I L E
2701 ACCAATCAACAGAATTTTTATCCTTCCAAGATGCCAGCTCATTGTACAGAAACATTTTAG
762   K E R E L Q Q L G I T E Y L R K N I A Q
2761 AAAAAGAAAGGGAACCTTCAGCAACTGGGAATCACAGAATACCTAAGGAAAAACATTGCTC
782   L Q P D M E A H Y P G A H E E L K L M E
2821 AGCTCCAGCCTGATATGGAGGCACATTATCCTGGAGCCCACGAAGAGCTGAAGTTAATGG
802   T L M Y S R P R K V L V E Q T K N E Y F
2881 AAACATTAATGTACTCACGTCCAAGGAAGGTATTAGTGGAACAGACAAAAAATGAGTATT
822   E L K A N L H A E P D Y L E V L E Q Q T
2941 TTGAACTTAAAGCTAATTTACATGCTGAACCTGACTATTTAGAAGTCCTGGAGCAGCAAA
842   *
3001 CATAGatggagaggttgagggctttcgccagaaatgctgtgattctgttattaagtccata
3061 ccttgtaaataagtgcccttacgtgagtggtgtcatcaatcagaacctaagcacagagtaaa
3121 ctatggggaaaaaaaaaagaagacgaaacagaaaactcagggatcactgggagaagccatgg
3181 cataatcttcaggcaattttagtctgtcccaaataaacatacatccttggcatgtaaatca
3241 tcaagggtaatagtaatatcatatacctgaaacgtgtctcataggagtcctctctgcac

```

Figure 2F-1. The cDNA (SEQ ID NO:12) and amino acid sequence (SEQ ID NO:13) of 158P1D7 v.6.

The start methionine is underlined. The open reading frame extends from nucleic acid 23-1612 including the stop codon.

```

1           M K L W I H L F Y S S L L
1 tcggatttcatcacatgacaacATGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCT
14 A C I S L H S Q T P V L S S R G S C D S
61 TGCCTGTATATCTTTACACTCCCAAACTCCAGTGCTCTCATCCAGAGGCTCTTGATTC
34 L C N C E E K D G T M L I N C E A K G I
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAAGGTAT
54 K M V S E I S V P P S R P F Q L S L L N
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAATAAGCTTATTAAA
74 N G L T M L H T N D F S G L T N A I S I
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT
94 H L G F N N I A D I E I G A F N G L G L
301 ACACCTTGGATTTTACAATATTGCAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCT
114 L K Q L H I N H N S L E I L K E D T F R

```

Figure 2F-2

361 CCTGAAACAACCTTCATATCAATCACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCA
 134 G L E N L E F L Q A D N N F I T V I E P
 421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
 154 S A F S K L N R L K V L I L N D N A I E
 481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
 174 S L P P N I F R F V P L T H L D L R G N
 541 GAGTCTTCCTCCAAACATCTTCCGATTTGTTCTTTAACCCATCTAGATCTTCGTGGAAA
 194 Q L Q T L P Y V G F L E H I G R I L D L
 601 TCAATTACAAACATTGCCTTATGTTGGTTTTCTCGAACACATTGGCCGAATATTGGATCT
 214 Q L E D N K W A C N C D L L Q L K T W L
 661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT
 234 E N M P P Q S I I G D V V C N S P P F F
 721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTTT
 254 K G S I L S R L K K E S I C P T P P V Y
 781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
 274 E E H E D P S G S L H L A A T S S I N D
 841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
 294 S R M S T K T T S I L K L P T K A P G L
 901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACCTACCCACCAAAGCACCAGGTTT
 314 I P Y I T K P S T Q L P G P Y C P I P C
 961 GATACCTTATATTACAAAGCCATCCACTCAACTCCAGGACCTTACTGCCCTATTCCTTG
 334 N C K V L S P S G L L I H C Q E R N I E
 1021 TAACTGCAAAGTCCTATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA
 354 S L S D L R P P P Q N P R K L I L A G N
 1081 AAGCTTATCAGATCTGAGACCTCCTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGGAAA
 374 I I H S L M N P S F G P K H L E E E E E
 1141 TATTATTCACAGTTTAATGAATCCATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGA
 394 R N E K E G S D A K H L Q R S L L E Q E
 1201 GAGGAATGAGAAAGAAGGAAGTGATGCAAAACATCTCCAAAGAAGTCTTTTGGAACAGGA
 414 N H S P L T G S N M K Y K T T N Q S T E
 1261 AAATCATTCACTCACTCACAGGGTCAAATATGAAATACAAAACCACGAACCAATCAACAGA
 434 F L S F Q D A S S L Y R N I L E K E R E
 1321 ATTTTTATCCTTCCAAGATGCCAGCTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGA
 454 L Q Q L G I T E Y L R K N I A Q L Q P D
 1381 ACTTCAGCAACTGGGAATCACAGAATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGA
 474 M E A H Y P G A H E E L K L M E T L M Y
 1441 TATGGAGGCACATTATCCTGGAGCCCACGAAGAGCTGAAGTTAATGGAAACATTAATGTA
 494 S R P R K V L V E Q T K N E Y F E L K A
 1501 CTCACGTCCAAGGAAGGTATTAGTGGAACAGACAAAAAATGAGTATTTTGAACCTAAAGC

Figure 2F-3

514 N L H A E P D Y L E V L E Q Q T *
1561 TAATTTACATGCTGAACCTGACTATTTAGAAGTCCTGGAGCAGCAAACATAGatggaga

Figure 3:

Figure 3A. Amino acid sequence 158P1D7 v.1 (SEQ ID NO:14). The 158P1D7 v.1 protein has 841 amino acids.

```
1 MKLWIHLFYS SLLACISLHS QTPVLSSRGS CDSLNCCEEK DGTMLINCEA KGIKMOVSEIS
61 VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIH LGFN NI ADIEIGAFNG LGLLKQLHIN
121 HNSLEILKED TFHGLENLEF LQADNNFITV IEPSAFSKLN RLKVLILNDN AIESLPPNIF
181 RFVPLTHLDL RGNQLQTLPY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT
301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP
361 PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGSFMNL TRLQKLYLNG
421 NHLTKLSKGM FLGLHNLEYL YLEYNAIKEI LPGTFNMPK LKVLYLNNNL LQVLPPHIFS
481 GVPLTKVNLK TNQFTHLPVS NILDDL DLLT QIDLEDNPWD CSCDLVGLQQ WIQKLSKNTV
541 TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSMPTQTS YLMVTTTATT TNTADTILRS
601 LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM
661 YGHKTTHHTT ERPSASLYEQ H MVSPMVHVY RSPSFGPKHL EEEEEERNEKE GSDAKHLQRS
721 LLEQENHSPL TGSNMKYKTT NQSTEF LSFQ DASSLYRNIL EKERELQQLG ITEYLRKNIA
781 QLQPDMEAHY PGAHEELKLM ETLMYSRPRK VLVEQTKNEY FELKANLHAE PDYLEVLEQQ
841 T
```

Figure 3B. Amino acid sequence 158P1D7 v.3 (SEQ ID NO:15). The 158P1D7 v.3 protein has 732 amino acids.

```
1 MKLWIHLFYS SLLACISLHS QTPVLSSRGS CDSLNCCEEK DGTMLINCEA KGIKMOVSEIS
61 VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIH LGFN NI ADIEIGAFNG LGLLKQLHIN
121 HNSLEILKED TFHGLENLEF LQADNNFITV IEPSAFSKLN RLKVLILNDN AIESLPPNIF
181 RFVPLTHLDL RGNQLQTLPY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT
301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP
361 PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGSFMNL TRLQKLYLNG
421 NHLTKLSKGM FLGLHNLEYL YLEYNAIKEI LPGTFNMPK LKVLYLNNNL LQVLPPHIFS
481 GVPLTKVNLK TNQFTHLPVS NILDDL DLLT QIDLEDNPWD CSCDLVGLQQ WIQKLSKNTV
541 TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSMPTQTS YLMVTTTATT TNTADTILRS
601 LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM
661 YGHKTTHHTT ERPSASLYEQ HMGAEHEELKL METLMYSRPR KVLVEQTKNE YFELKANLHA
721 EPDYLEVLEQ QT
```

Figure 3C. Amino acid sequence 158P1D7 v.4 (SEQ ID NO:16). The 158P1D7 v.4 protein has 395 amino acids.

```
1  MKLWIHLFYS  SLLACISLHS  QTPVLSSRGS  CDSLNCNEEK  DGTMLINCEA  KGIKMOVSEIS
61  VPPSRPFQLS  LLNNGLTMLH  TNDFSGLTNA  ISIHLCGFNNI  ADIEIGAFNG  LGLLKQLHIN
121 HNSLEILKED  TFHGLENLEF  LQADNNFITV  IEPSAFSKLN  RLKVLILNDN  AIESLPPNIF
181 RFVPLTHLDL  RGNQLQTLPY  VGFLEHIGRI  LDLQLEDNKW  ACNCDLLQLK  TWLENMPPQS
241 IIGDVVCNSP  PFFKGSILSR  LKKESICPTP  PVYEEHEDPS  GSLHLAATSS  INDSRMSTKT
301 TSILKLPTKA  PGLIPYITKP  STQLPGPYCP  IPCNCKVLSP  SGLLIHCQER  NIESLSDLRP
361 PPQNPRKLIL  AGNIIHSLMK  SILWSKASGR
```

Figure 3D. Amino acid sequence 158P1D7 v.6 (SEQ ID NO:17). The 158P1D7 v.6 protein has 529 amino acids.

```
1  MKLWIHLFYS  SLLACISLHS  QTPVLSSRGS  CDSLNCNEEK  DGTMLINCEA  KGIKMOVSEIS
61  VPPSRPFQLS  LLNNGLTMLH  TNDFSGLTNA  ISIHLCGFNNI  ADIEIGAFNG  LGLLKQLHIN
121 HNSLEILKED  TFHGLENLEF  LQADNNFITV  IEPSAFSKLN  RLKVLILNDN  AIESLPPNIF
181 RFVPLTHLDL  RGNQLQTLPY  VGFLEHIGRI  LDLQLEDNKW  ACNCDLLQLK  TWLENMPPQS
241 IIGDVVCNSP  PFFKGSILSR  LKKESICPTP  PVYEEHEDPS  GSLHLAATSS  INDSRMSTKT
301 TSILKLPTKA  PGLIPYITKP  STQLPGPYCP  IPCNCKVLSP  SGLLIHCQER  NIESLSDLRP
361 PPQNPRKLIL  AGNIIHSLMN  PSFGPKHLEE  EEERNEKEGS  DAKHLQRSLL  EQENHSPLTG
421 SNMKYKTTNQ  STEFLSFQDA  SSLYRNILEK  ERELQQLGIT  EYLRKNIAQL  QPDMEAHYPG
481 AHEELKLMET  LMYSRPRKVL  VEQTKNEYFE  LKANLHAEPD  YLEVLEQQT
```


Figure 4: 158P1D7 v.1 amino acid (SEQ ID NO:18) BLAST homology to hypothetical protein FLJ22774 (SEQ ID NO:19).

Identities = 798/798 (100%)

```
Query: 44  MLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIH LGFN NIADI 103
          MLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIH LGFN NIADI
Sbjct: 1   MLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIH LGFN NIADI 60

Query: 104 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 163
          EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK
Sbjct: 61  EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 120

Query: 164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPYVGFLEHIGRILDQLQEDN KWACN 223
          VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPYVGFLEHIGRILDQLQEDN KWACN
Sbjct: 121 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPYVGFLEHIGRILDQLQEDN KWACN 180

Query: 224 CDLLQLK TWLENMPPQSIIGDVVCNSPPFFKGSILSR LKKESICPTPPVYEEHEDPSGSL 283
          CDLLQLK TWLENMPPQSIIGDVVCNSPPFFKGSILSR LKKESICPTPPVYEEHEDPSGSL
Sbjct: 181 CDLLQLK TWLENMPPQSIIGDVVCNSPPFFKGSILSR LKKESICPTPPVYEEHEDPSGSL 240

Query: 284 HLAATSSINDSRMSTKTTT SILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 343
          HLAATSSINDSRMSTKTTT SILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL
Sbjct: 241 HLAATSSINDSRMSTKTTT SILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 300

Query: 344 LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGN NR IEVLE 403
          LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGN NR IEVLE
Sbjct: 301 LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGN NR IEVLE 360

Query: 404 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAI KEILPGTFNMPMKLV 463
          EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAI KEILPGTFNMPMKLV
Sbjct: 361 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAI KEILPGTFNMPMKLV 420

Query: 464 LYLNNNLLQVLPPHIFSGVPLTKVNLKTNQFTHLPVSNILDDL DLTQIDLEDNPDWCSC 523
          LYLNNNLLQVLPPHIFSGVPLTKVNLKTNQFTHLPVSNILDDL DLTQIDLEDNPDWCSC
Sbjct: 421 LYLNNNLLQVLPPHIFSGVPLTKVNLKTNQFTHLPVSNILDDL DLTQIDLEDNPDWCSC 480

Query: 524 DLVGLQQW IQKLSKNTVTDDILCTSPGHLDKKE LKALNSEILCPGLVNNPSMPTQT SYLM 583
          DLVGLQQW IQKLSKNTVTDDILCTSPGHLDKKE LKALNSEILCPGLVNNPSMPTQT SYLM
Sbjct: 481 DLVGLQQW IQKLSKNTVTDDILCTSPGHLDKKE LKALNSEILCPGLVNNPSMPTQT SYLM 540

Query: 584 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLV LHRRRRYKKKQ 643
          VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLV LHRRRRYKKKQ
Sbjct: 541 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLV LHRRRRYKKKQ 600

Query: 644 VDEQMRDN SPVHLQYS MYGHKTTHHTTERPSASLYEQH MVSPMVHVYRSPSFGPKHLEEE 703
          VDEQMRDN SPVHLQYS MYGHKTTHHTTERPSASLYEQH MVSPMVHVYRSPSFGPKHLEEE
Sbjct: 601 VDEQMRDN SPVHLQYS MYGHKTTHHTTERPSASLYEQH MVSPMVHVYRSPSFGPKHLEEE 660

Query: 704 EERNEKEGSDAKHLQRSLL EQENHSPLTGSNMKYKTTNQSTEF LSFQDASSLYRNILEKE 763
          EERNEKEGSDAKHLQRSLL EQENHSPLTGSNMKYKTTNQSTEF LSFQDASSLYRNILEKE
Sbjct: 661 EERNEKEGSDAKHLQRSLL EQENHSPLTGSNMKYKTTNQSTEF LSFQDASSLYRNILEKE 720

Query: 764 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL 823
          RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL
Sbjct: 721 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL 780

Query: 824 KANLHAEPDYLEVLEQQT 841
          KANLHAEPDYLEVLEQQT
Sbjct: 781 KANLHAEPDYLEVLEQQT 798
```

Figure 5:

Figure 5A: Alignment of 158P1D7 v.1 (SEQ ID NO:20) with human FLJ22774, CLONE KAIA1575.[Homo sapiens] (SEQ ID NO:21).

Identities = 405/415 (97%), Positives = 405/415 (97%)

```
158P1D7: 44 MLINCEAKGIKMVSEISVPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 103
              MLINCEAKGIKMVSEISVPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI
Sbjct: 1      MLINCEAKGIKMVSEISVPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 60

158P1D7:104 EIGAFNGLGLLKQLHINHNLSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLK 163
              EIGAFNGLGLLKQLHINHNLSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLK
Sbjct: 61     EIGAFNGLGLLKQLHINHNLSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLK 120

158P1D7:164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLHIGRILDQLQLEDNKWACN 223
              VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLHIGRILDQLQLEDNKWACN
Sbjct: 121    VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLHIGRILDQLQLEDNKWACN 180

158P1D7:224 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL 283
              CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL
Sbjct: 181    CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL 240

158P1D7:284 HLAATSSINDSRMSTKTTSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 343
              HLAATSSINDSRMSTKTTSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL
Sbjct: 241    HLAATSSINDSRMSTKTTSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 300

158P1D7:344 LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVLE 403
              LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVLE
Sbjct: 301    LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVLE 360

158P1D7:404 EGSFMNLRQLKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXXXAIKEILPGTFNPM 458
              EGSFMNLRQLKLYLNGNHLTKLSKGMFLGLH                      AIKEILPGTFNPM
Sbjct: 361    EGSFMNLRQLKLYLNGNHLTKLSKGMFLGLHNLLEYLYLEYNAIKEILPGTFNPM 415
```

Figure 5B-1: Alignment of 158P1D7 v.1 protein (SEQ ID NO:22) with a human protein similar to IGFALS (SEQ ID NO:23).

Identities = 316/864 (36%), Positives = 459/864 (52%)

```
158P1D7:1      MKLWIHLFYSSLLACISLSHSQTPVLSSRGSCDSLNCCEKDGTMLINCEAKGIKMVSEIS 60
              M LW+ L S+L++ + S V ++C+C + + +NCE + +++
Sbjct: 17      MFLWLFLILSALISSTNADSDISV-----EICNVCSVSVENVLYVNCEKVSVYRPNQLK 71

158P1D7:61     VPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI EIGAFNGLGLLKQLHIN 120
              P S + L+ NN L +L+ N F ++A+S+HLG N + +IE GAF GL LKQLH+N
Sbjct: 72     PPWSNFYHLNFQNNFLNILYPNTFLNFSHAVSLHLGNNKLQNI EGGAFLGLSALKQLHLN 131

158P1D7:121    HNSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESLPPNIF 180
              +N L+IL+ DTF G+ENLE+LQAD N I IE AF+KL++LKVILNDN I LP NIF
Sbjct: 132    NNELKILRADTF LGIENLEYLQADYNLIK YIERGAFNKLHKLKVLILNDNLISFLPDNIF 191

158P1D7:181    RFVPLTHLDLRGNQLQTLPLYVGFLHIGRILDQLQLEDNKWACNCDLLQLKTWLENMPPQS 240
              RF LTHLD+RGN++Q LPY+G LEHIGR+++LQLEDN W C+CDLL LK WLENMP
Sbjct: 192    RFASLTHLDIRGNRIQKLPYIGVLEHIGRVVELQLEDNPWNCSCDLLPLKAWLENMPYNI 251

158P1D7:241    IIGDVVCNSPPFFKGSILSRKKESICP-----TPPVYEEHEDPSGSLHLAATS 289
              IG+ +C +P G +L K+ +CP PP E+ + + H TS
Sbjct: 252    YIGEAI CETPSDLYGRLLKETNKQELCPMG TGSDFDVRILPPSQLENGYTTPNGHTTQTS 311

158P1D7:290    SINDSRMSTKTTSILKLPTKAPGLI-----PYITKPSTQLPG-PYCPIPCNCKV- 337
              KTT+ P+K G++ I T++P CP PC CK
Sbjct: 312    LHRLVT KPPKTTN----PSKISGIVAGKALSNRNLSQIVSYQTRVPLTPCPAPCFCKTH 367

158P1D7:338    LSPSGLLIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNN 397
              S GL ++CQE+NI+S+S+L P P N +KL + GN I + SD ++ L++LHLG+N
```

Figure 5B-2

Sbjct: 368 PSDLGSLVNCQEKNIQSMSELIPKPLNAKKLHVNGNSIKDQDVSDFTDFEGLDLLHLGNS 427

158P1D7:398 RIEVLEEGSFMMNLTQLKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNP 457
+I V++ F NLT L++LYLNGN + +L +F GLH IKEI GTF+

Sbjct: 428 QITVIKGDVFNLTNLRLRLYLNGNQIERLYPEIFSGLHNLQYLYLEYNLIKEISAGTFDS 487

158P1D7:458 MXXXXXXXXXXXXXXXXXHFSGVPLTKVNLKTNQFTHLPVSNIXXXXXXXXXXXXXXN 517
M +IFSG PL ++NL+ N+F +LPVS + N

Sbjct: 488 MPNLQLLYLNNNLLKSLPVYIFSGAPLARLNLNRNNKFMYPVSGVLDQLQSLTQIDLEGN 547

158P1D7:518 PWDCSCDLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKELKALNSEILCPGLVNNPSMPT 577
PWDC+CDLV L+ W++KLS V ++ C +P ELK+L +EILCP L+N PS P

Sbjct: 548 PWDCTCDLVALKLWVEKLSDGIVVKELKCETPVQFANIELKSLKNEILCPKLLNKPSAP- 606

158P1D7:578 QTSYLMVXXXXXXXXXXXXXILRSLTDAVPLSVLILGLLLIMFITIVFCAAGIVVLVHRRR 637
+ I VPLS+LIL +L++ I VF A ++V VL R +

Sbjct: 607 ---FTSPAPAITFTTPLGPPIRSPPGPVPLSILILSVLILTVFVAFCLLVFVLRNRK 663

158P1D7:638 RYKKKQVDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHVMSPMVHVYRSPSFGP 697
+ K D + LQ + HK T + E + + +S + G

Sbjct: 664 KPTVKHEGLGNPDCGSMQLQLRKHDHK-----TNKKDGLSTEAFIPQTIEQMSKSHTCGL 718

158P1D7:698 KHLXXXXXXXXXXGSDAKHLQRSLLSEQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYR 757
K G K + R++ ++E + + T ++ E +D++ +

Sbjct: 719 KESETGFMFSDPPGQ--KVVMRNVADKEKDLLHVDTRKRLSTIDELDELFPSPRDSNVFIQ 776

158P1D7:758 NILEKERELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTK 817
N LE ++E +G++ + E YP + K ++L+ K++VEQ K

Sbjct: 777 NFLESKKEYNSIGVSGF-----EIRYPEKQPDKSKSKSLIGGNHISKIVVEQRK 824

158P1D7:818 NEYFELKANLHAEFDYLEVLEQQT 841
+EYFELKA L + PDYL+VLE+QT

Sbjct: 825 SEYFELKAKLQSSPDYLVLEEQT 848

Figure 6. Expression of 158P1D7 by RT-PCR

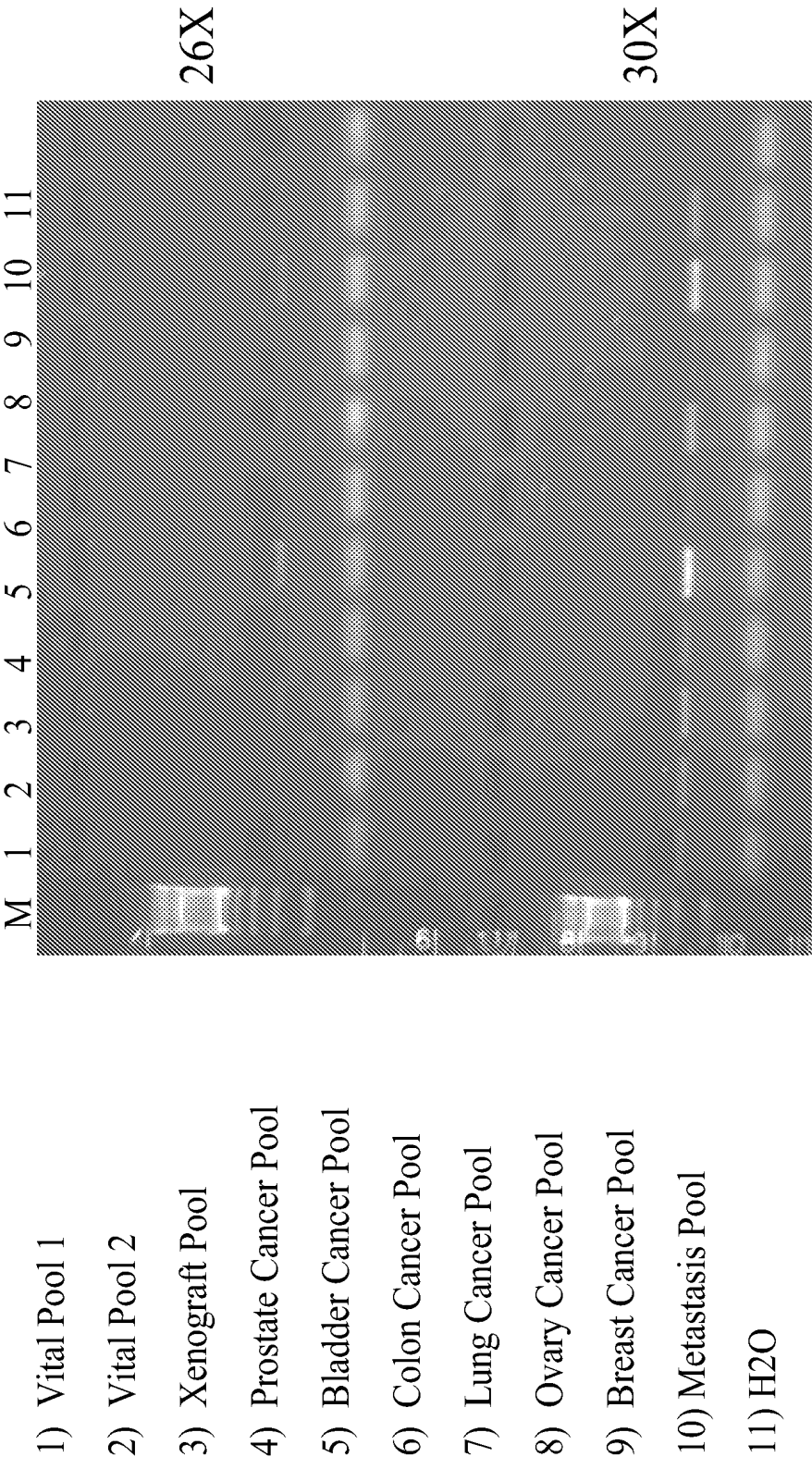


Figure 7. Expression of 158P1D7 in Normal Tissues

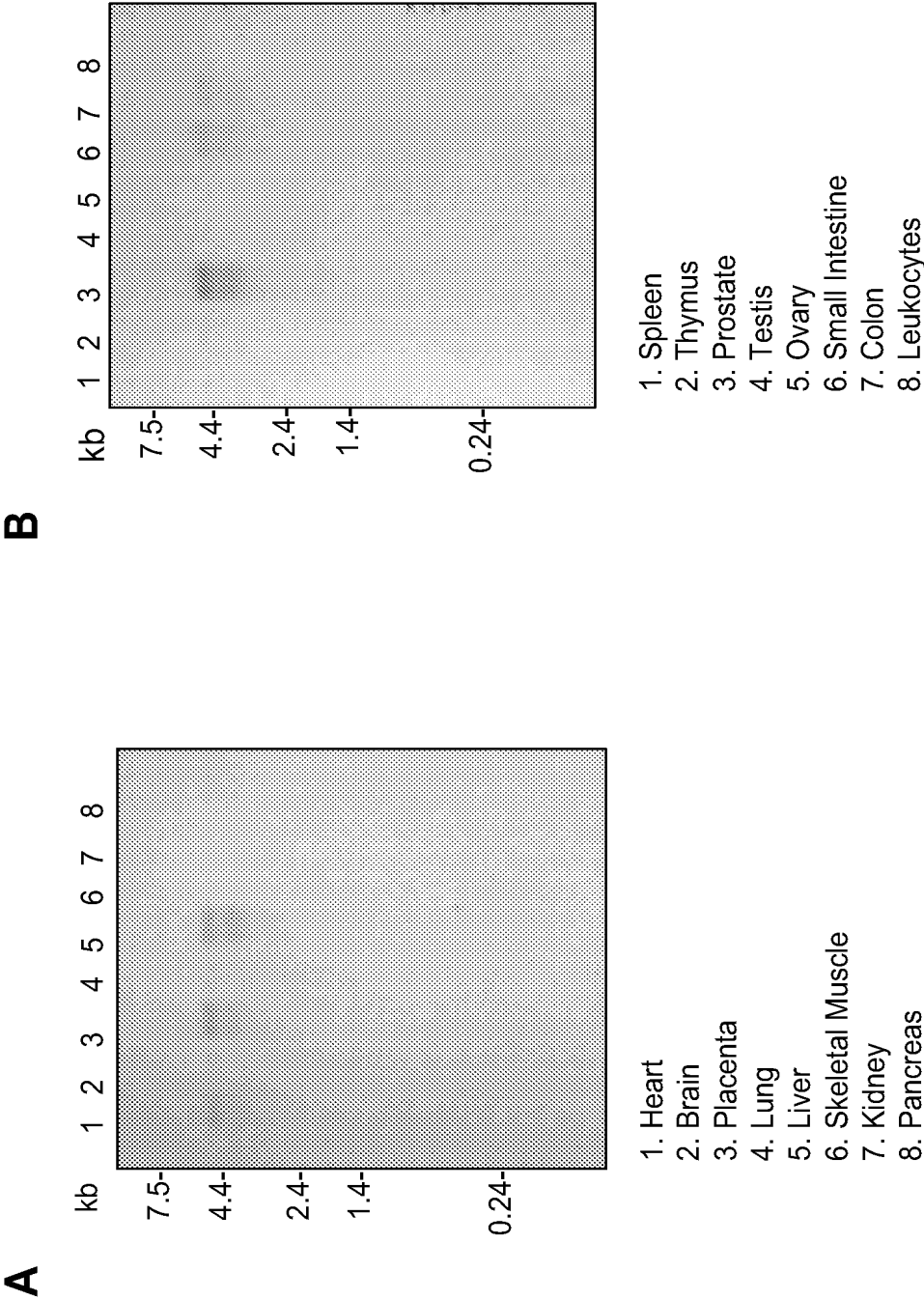


Figure 8A. Expression of 158P1D7 in Bladder Cancer Patient Specimens

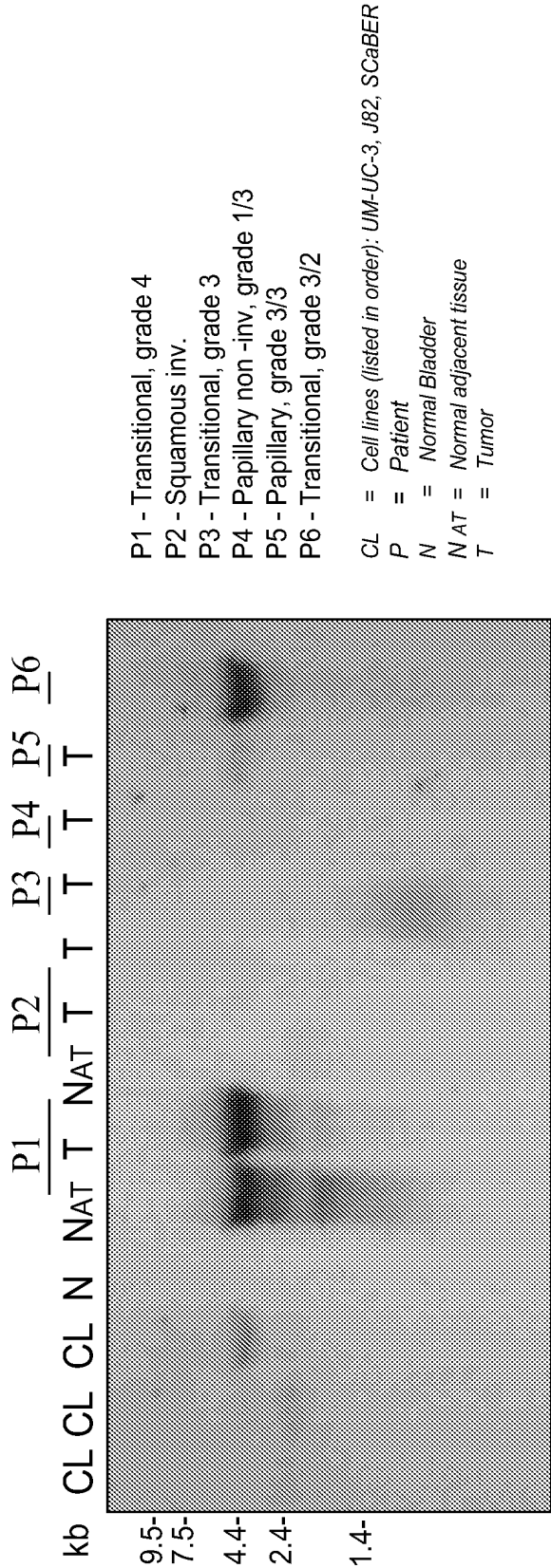


Figure 8B. Expression of 158P1D7 in Bladder Cancer Patient Specimens

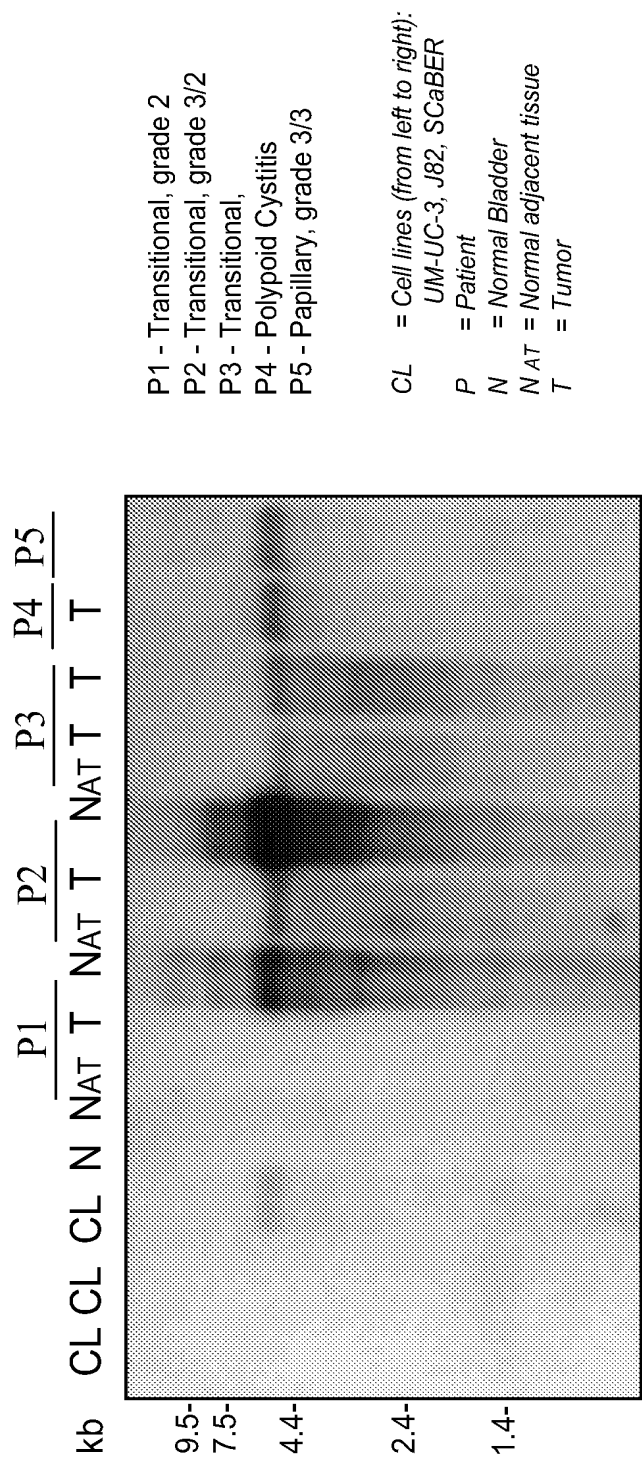


Figure 9. Expression of 158P1D7 in Lung Cancer Patient Specimens

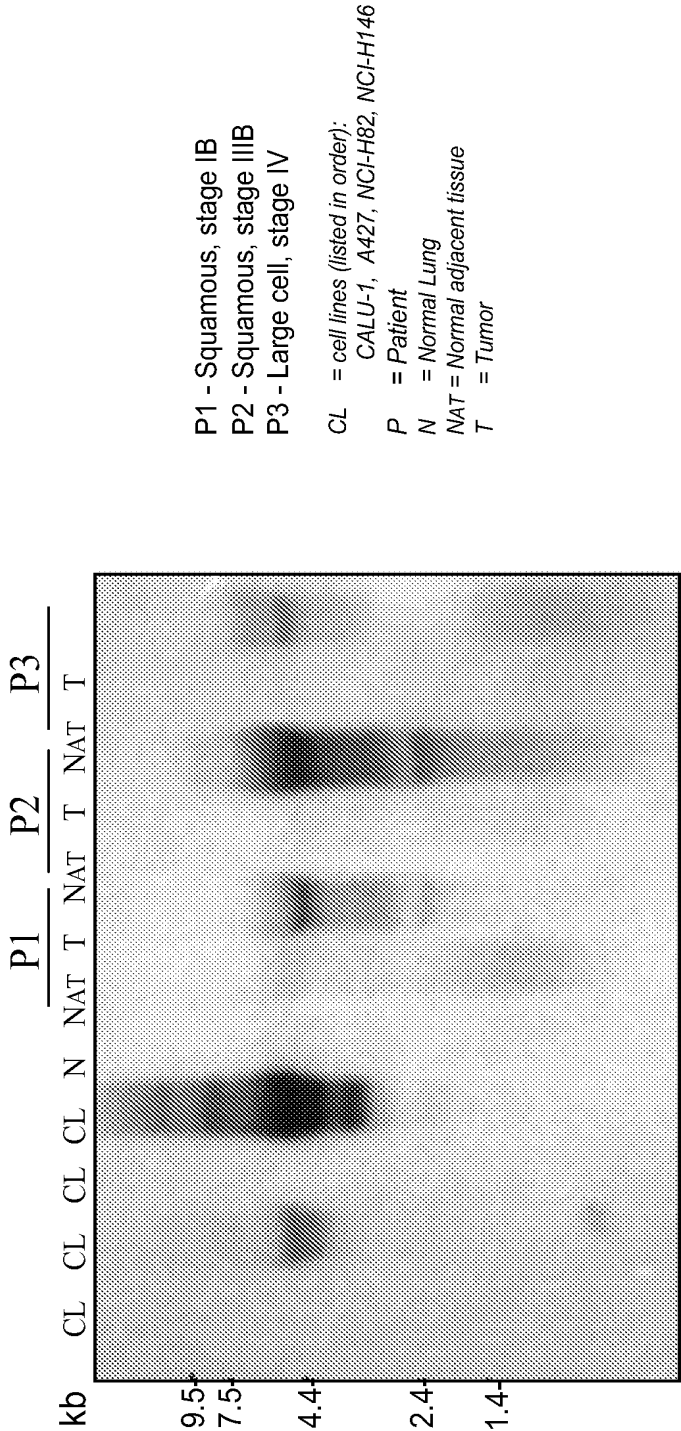


Figure 10. Expression of 158P1D7 in Breast Cancer Patient Specimens

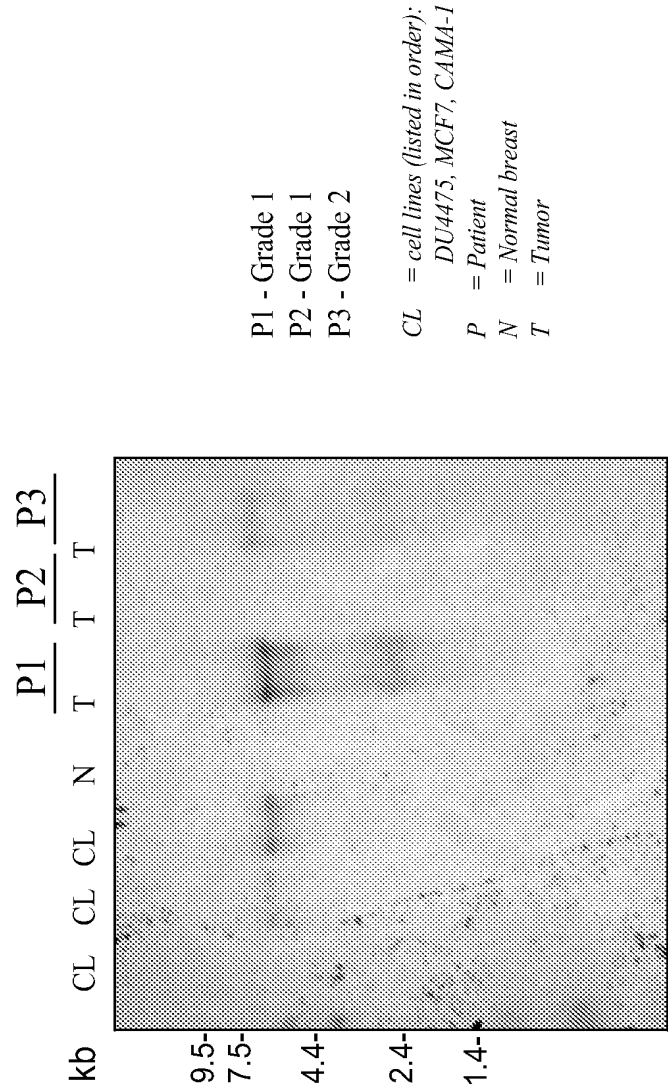


Figure 11a - 158P1D7 variant 1

Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

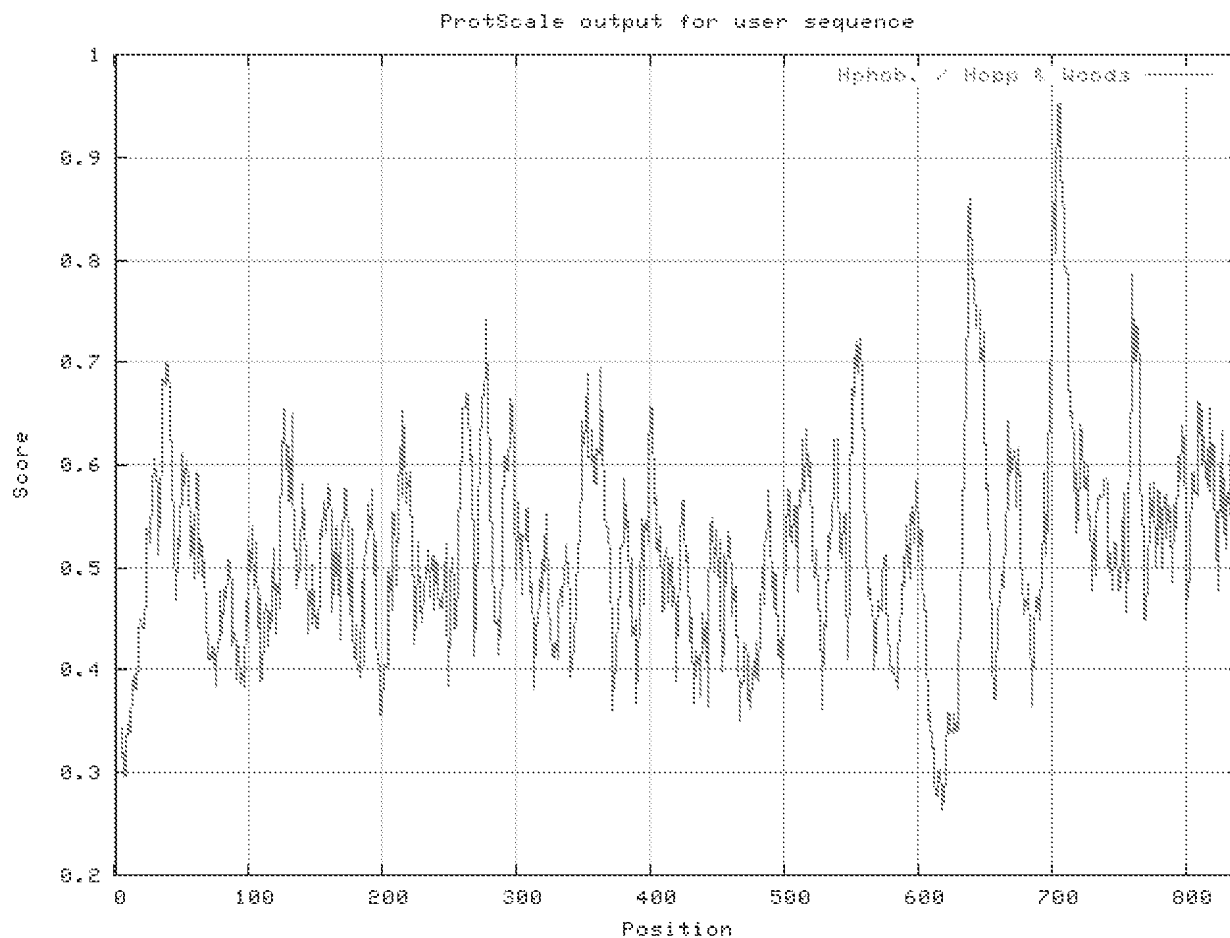


Figure 11b - 158P1D7 variant 3
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

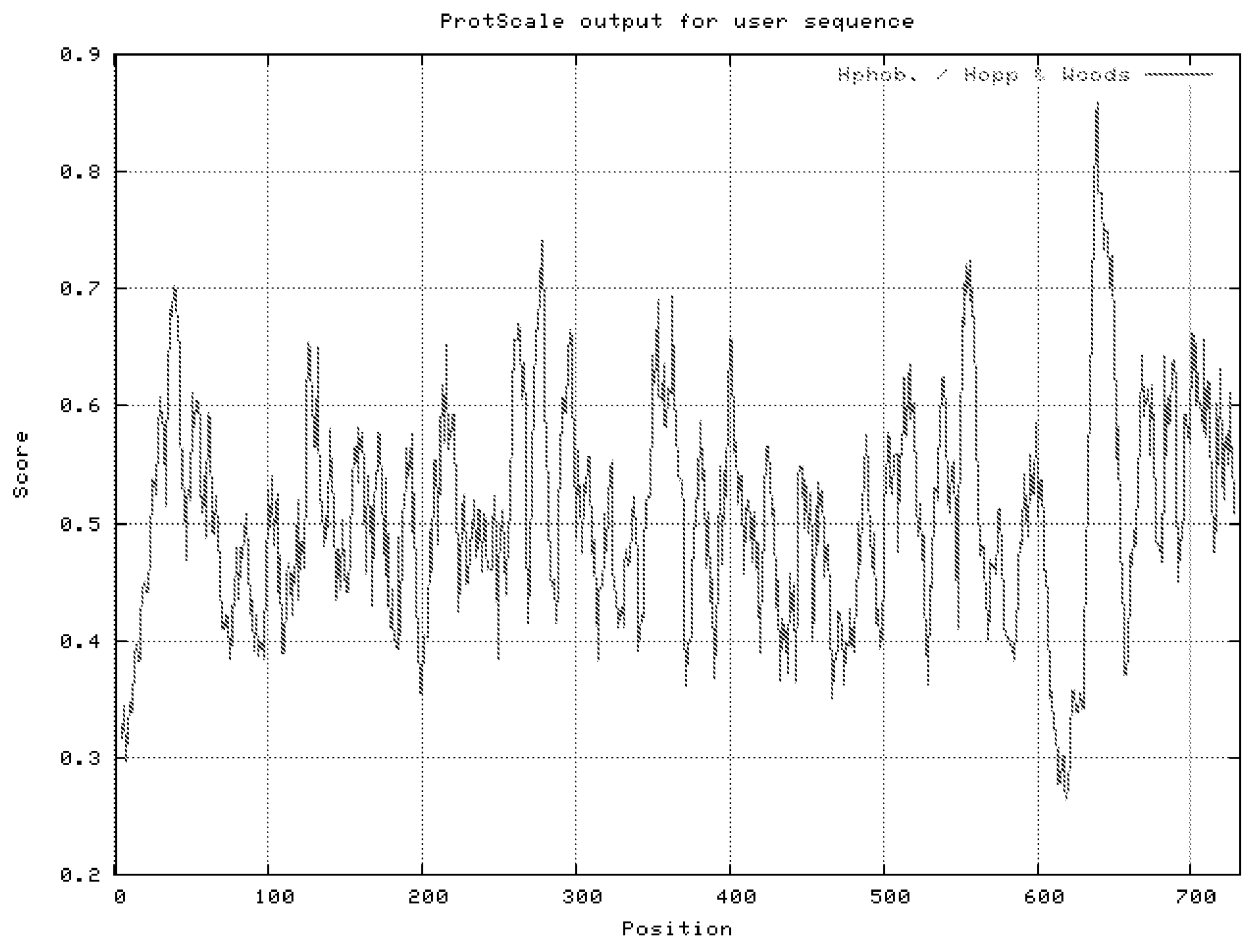


Figure 11c - 158P1D7 variant 4
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

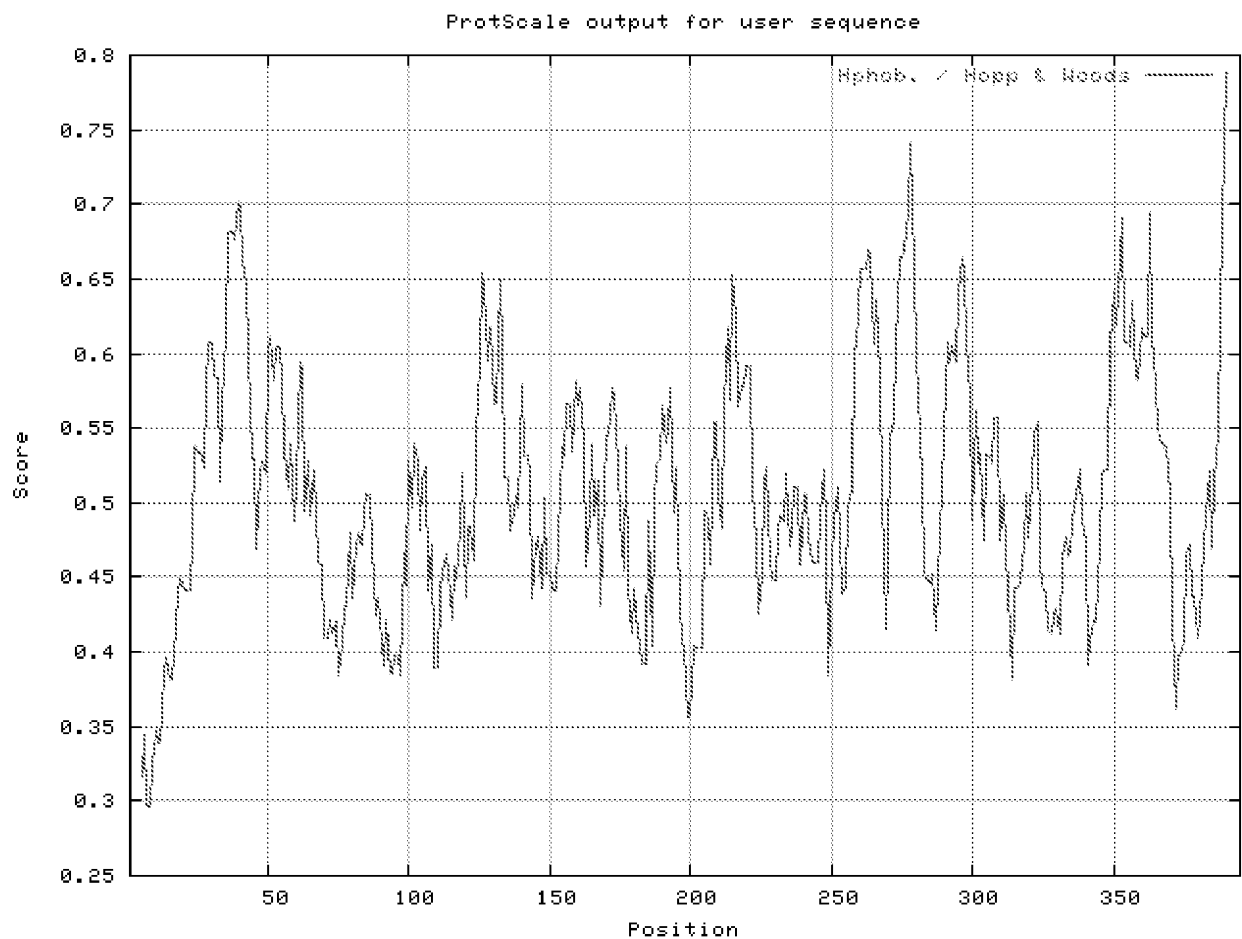


Figure 11d - 158P1D7 variant 6

Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

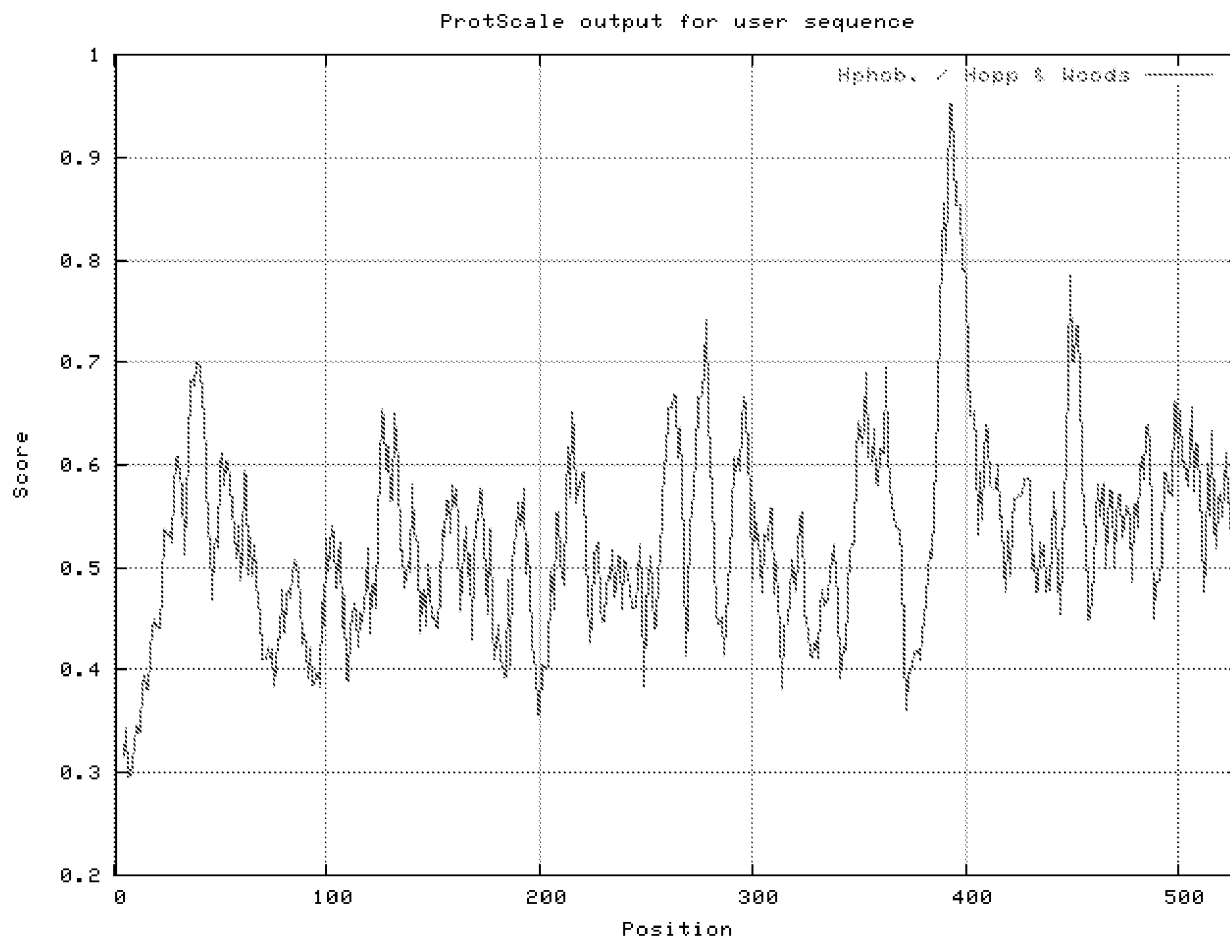


Figure 12a - 158P1D7 variant 1

Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

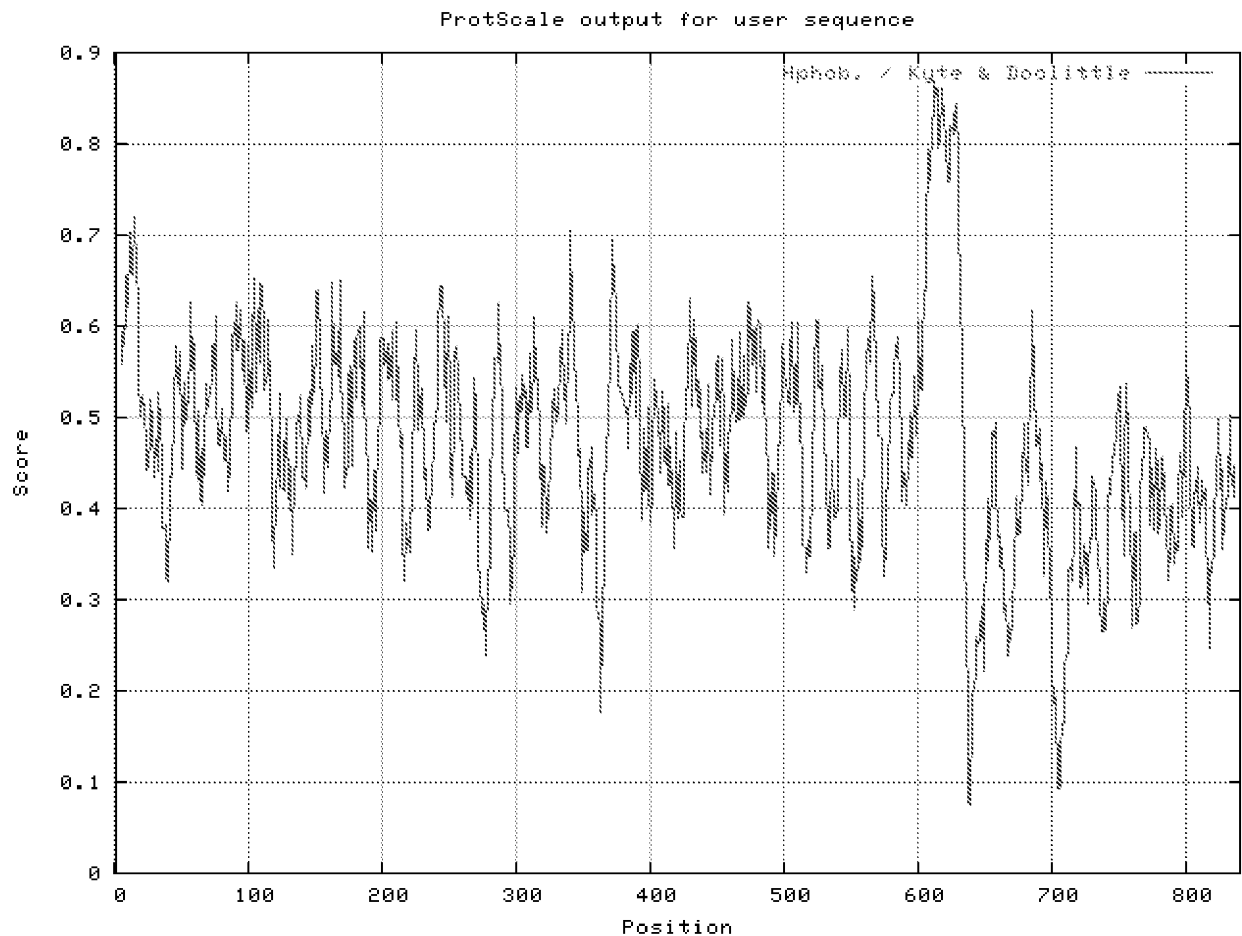


Figure 12b - 158P1D7 variant 3

Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

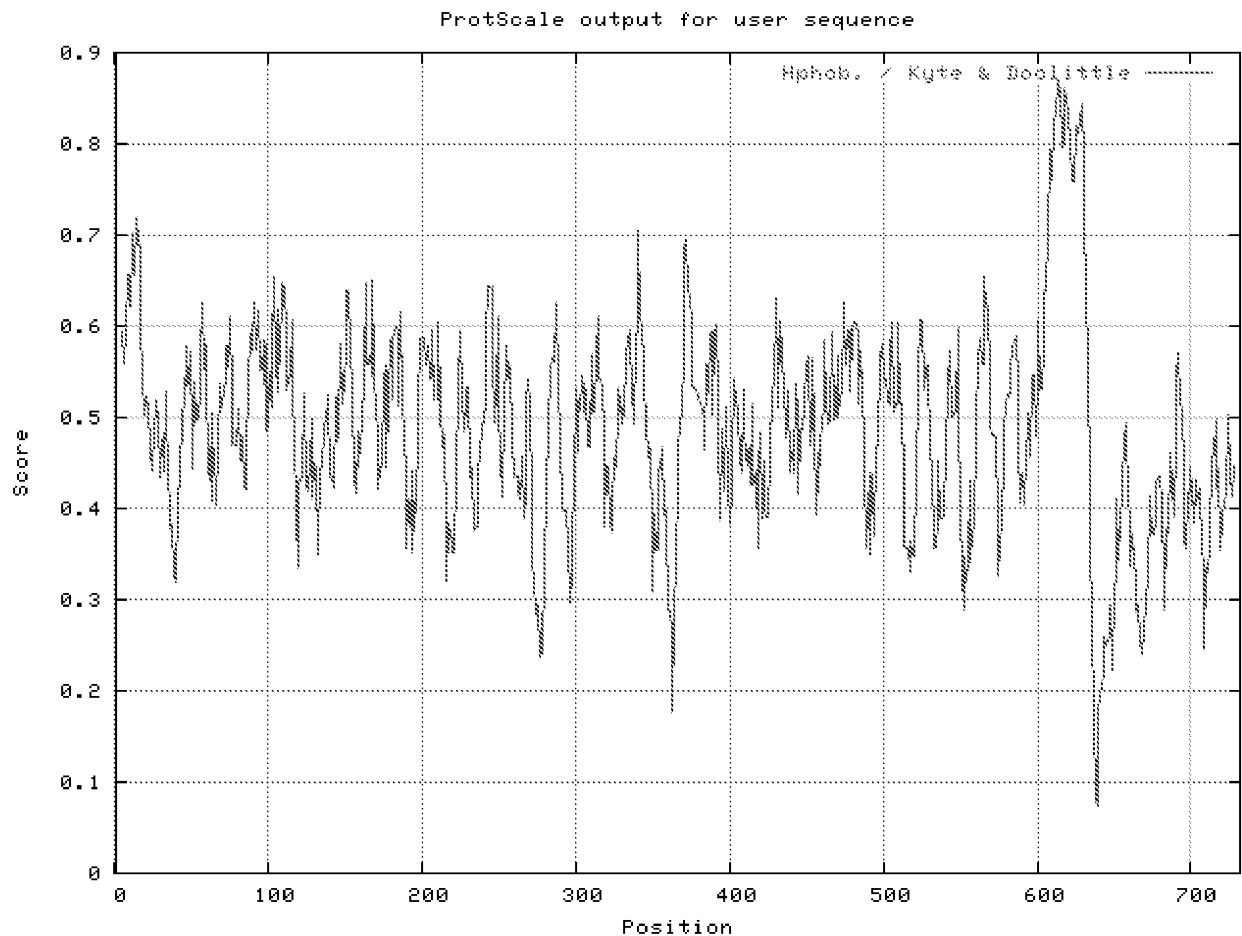


Figure 12c - 158P1D7 variant 4

Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

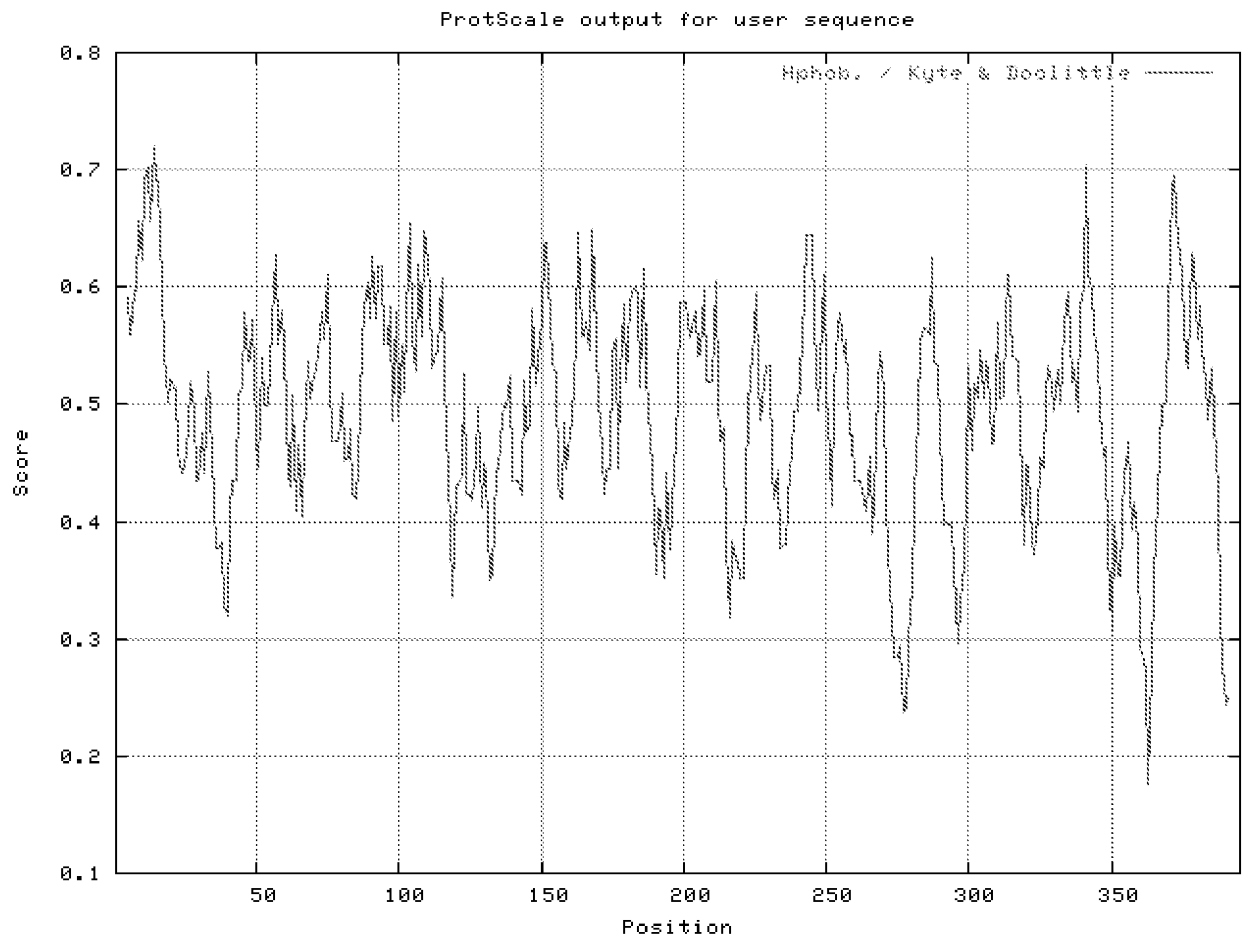


Figure 12d - 158P1D7 variant 6

Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

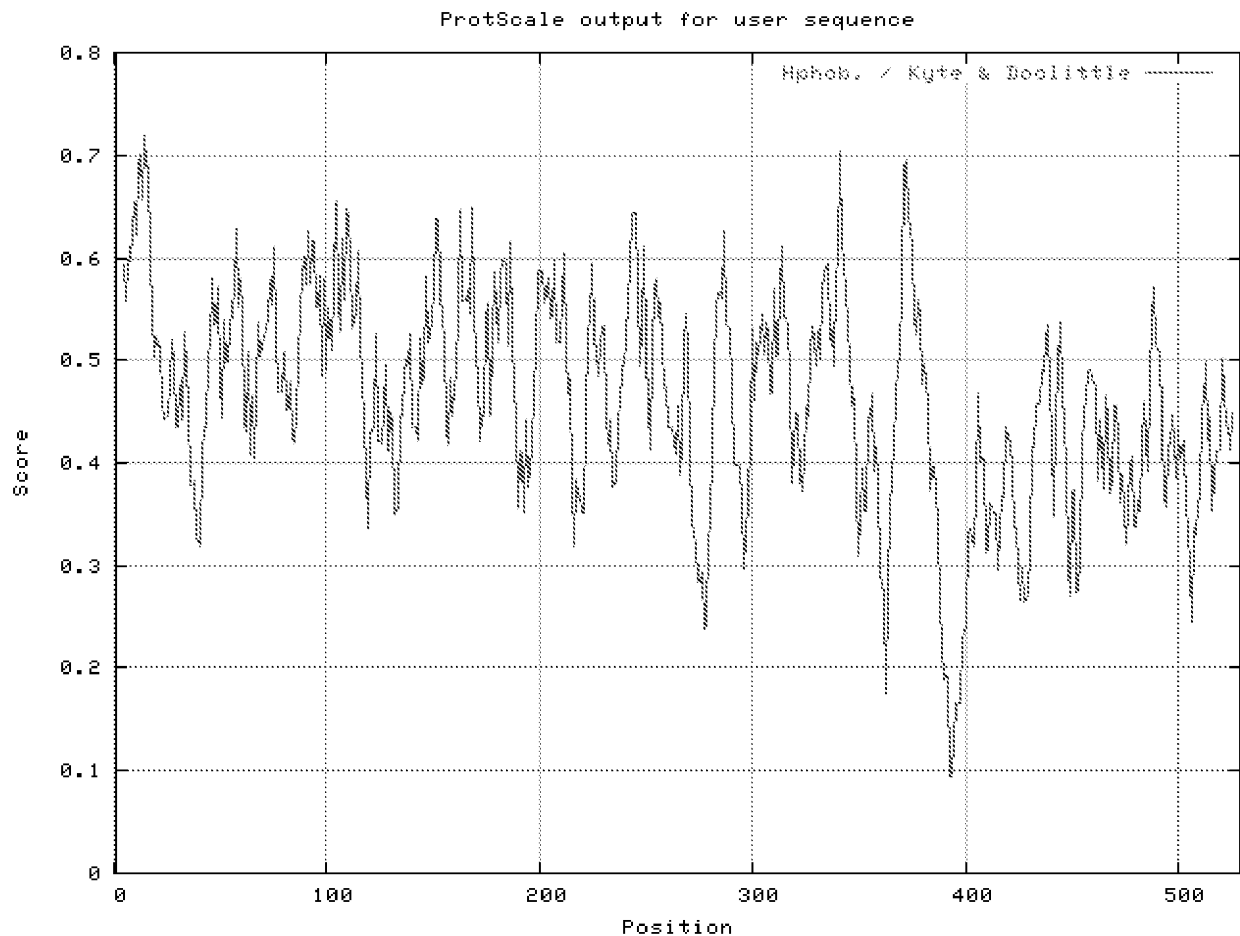


Figure 13a - 158P1D7 variant 1 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

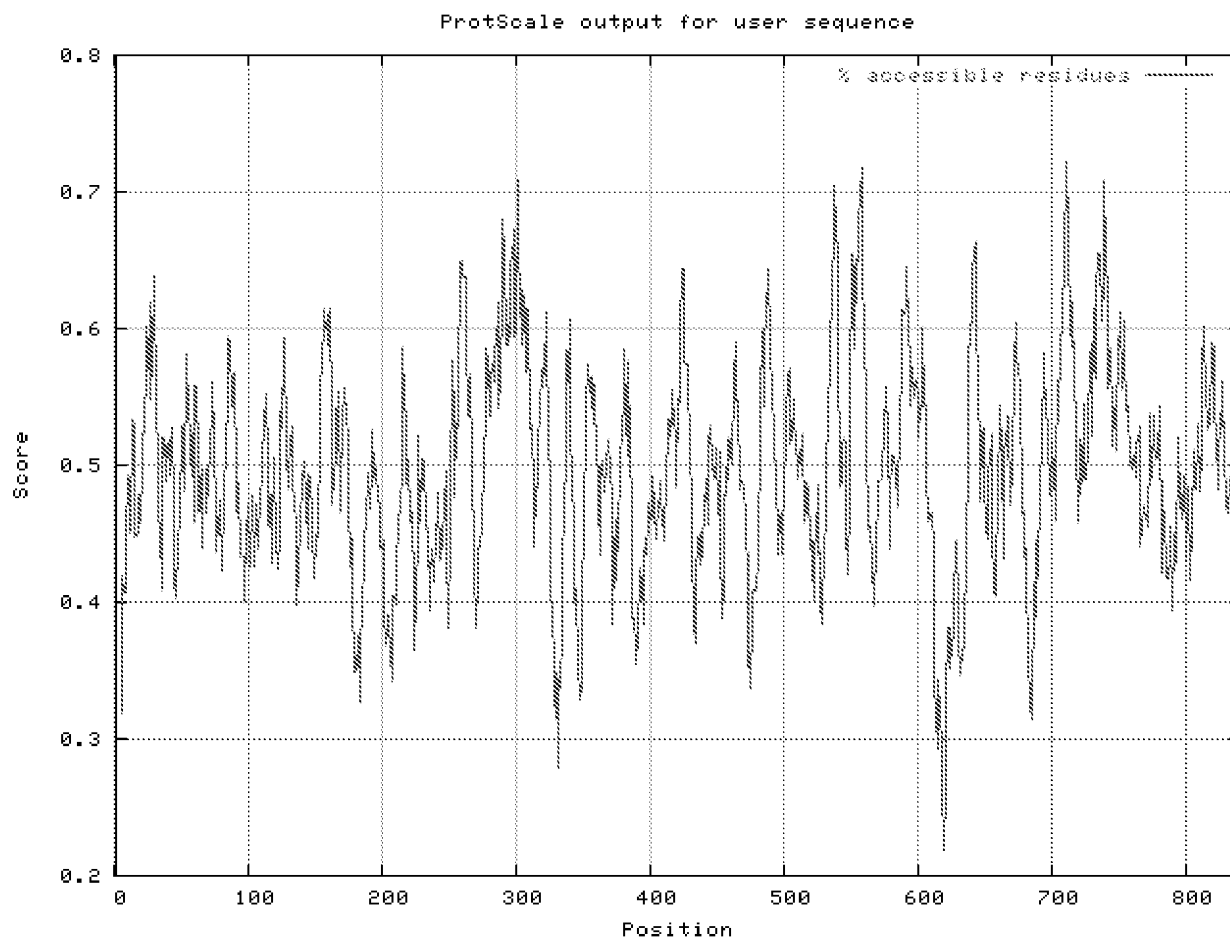


Figure 13b - 158P1D7 variant 3 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

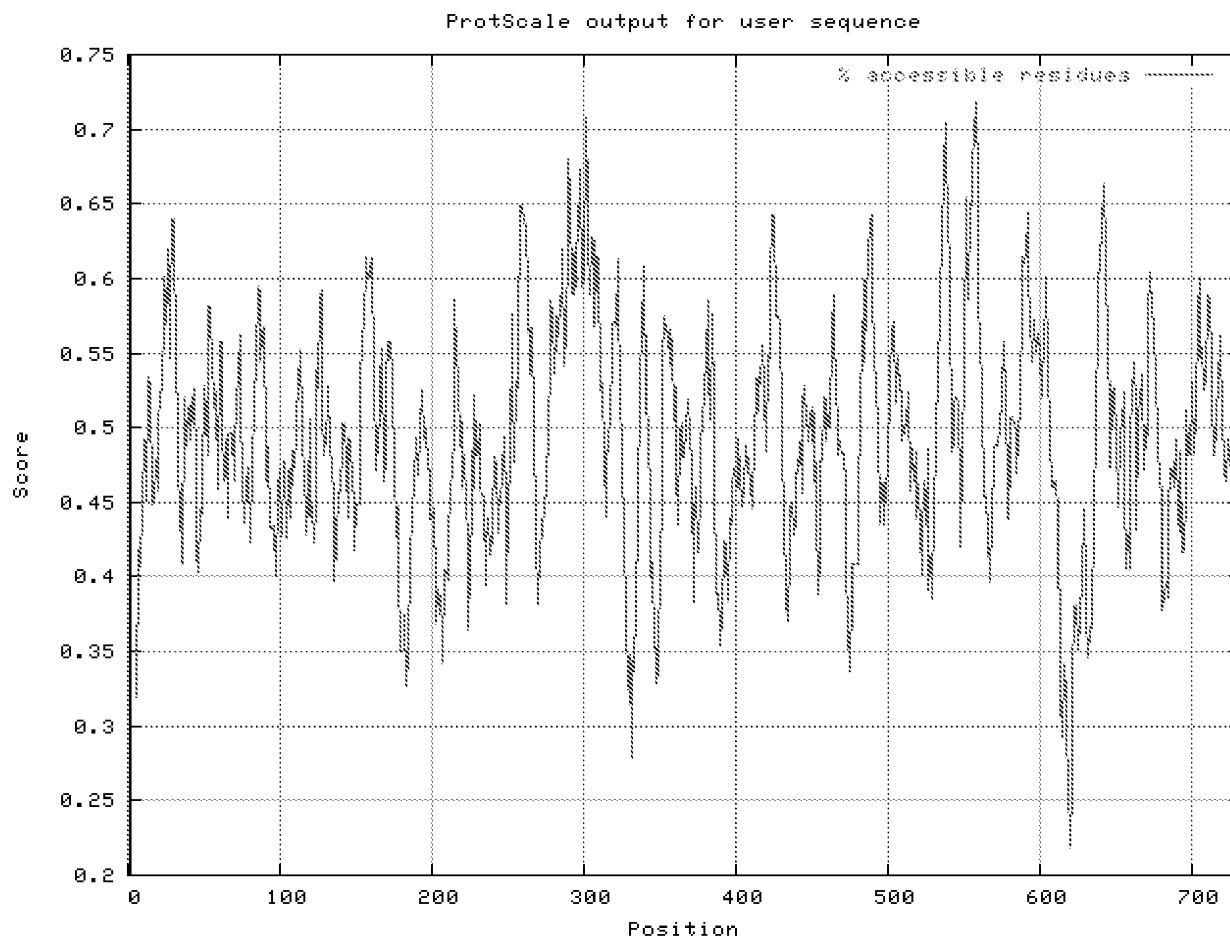


Figure 13c - 158P1D7 variant 4 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

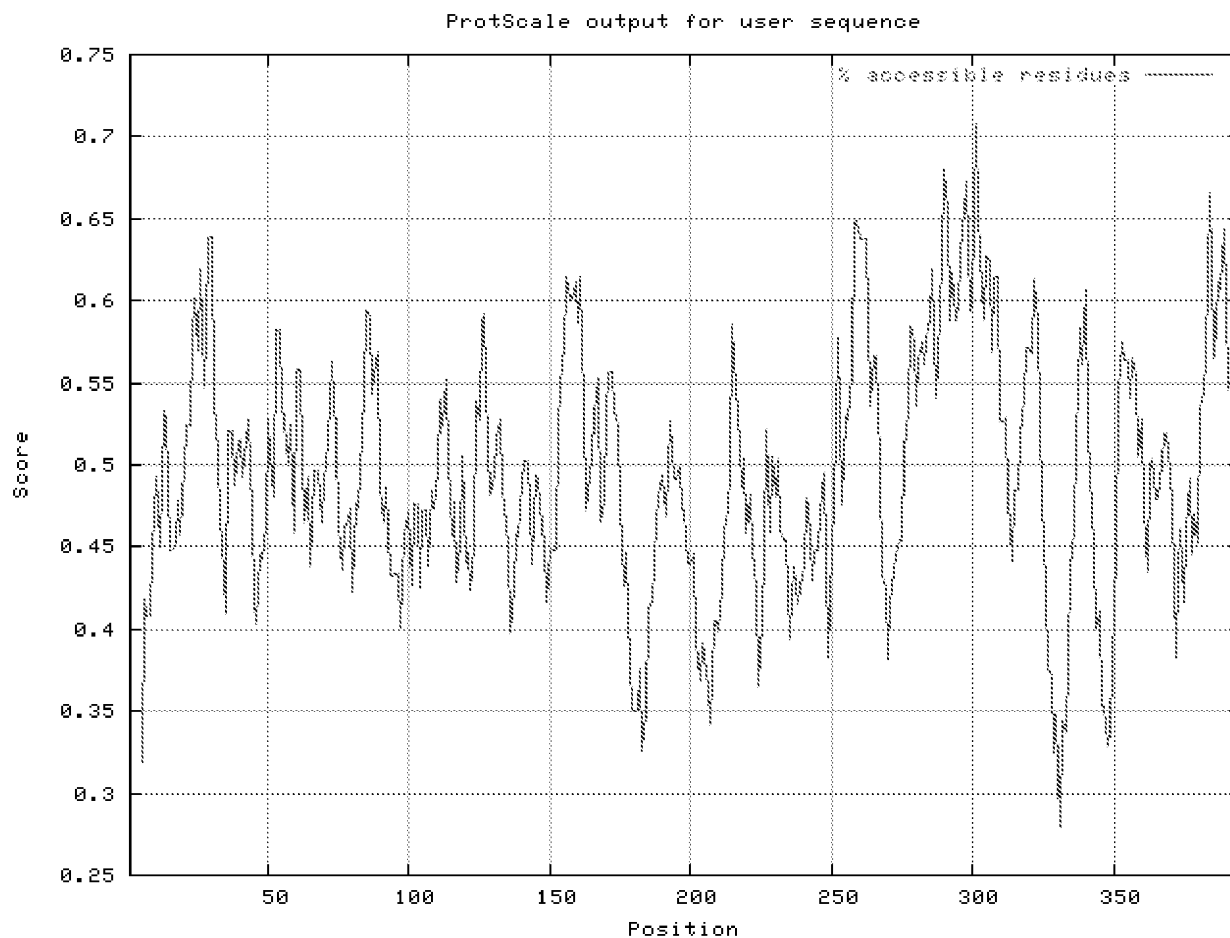


Figure 13d - 158P1D7 variant 6 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

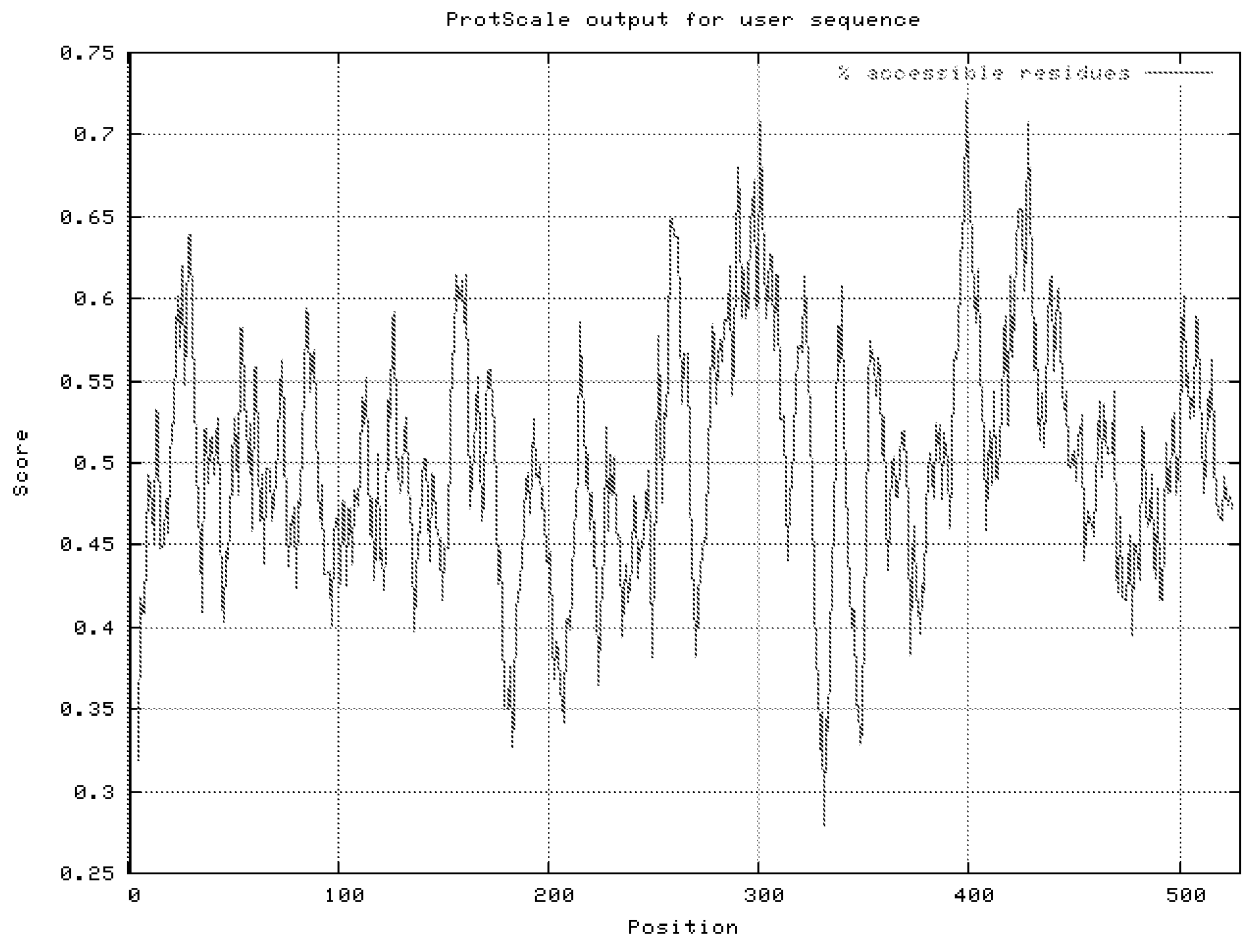


Figure 14a - 158P1D7 variant 1

Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

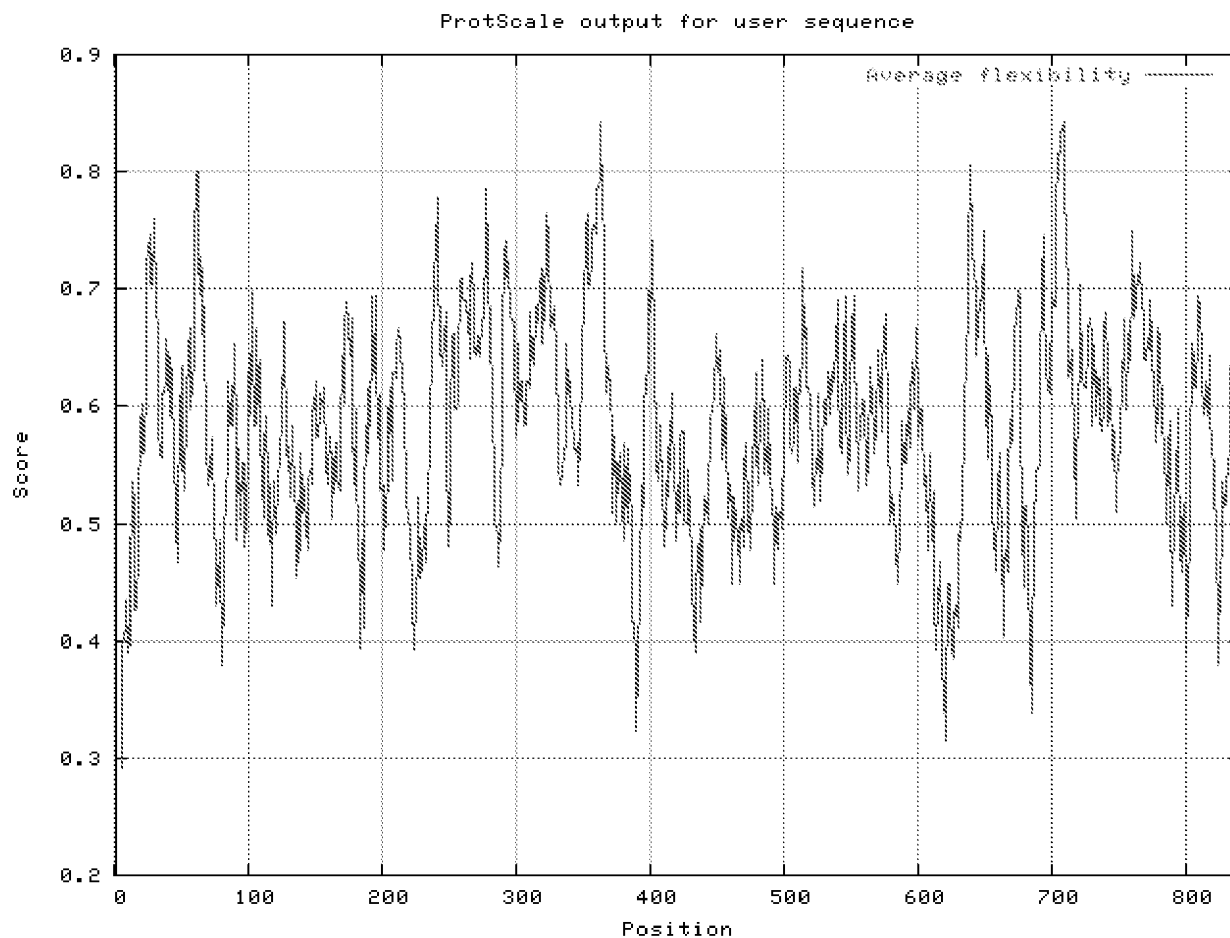


Figure 14b - 158P1D7 variant 3

Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

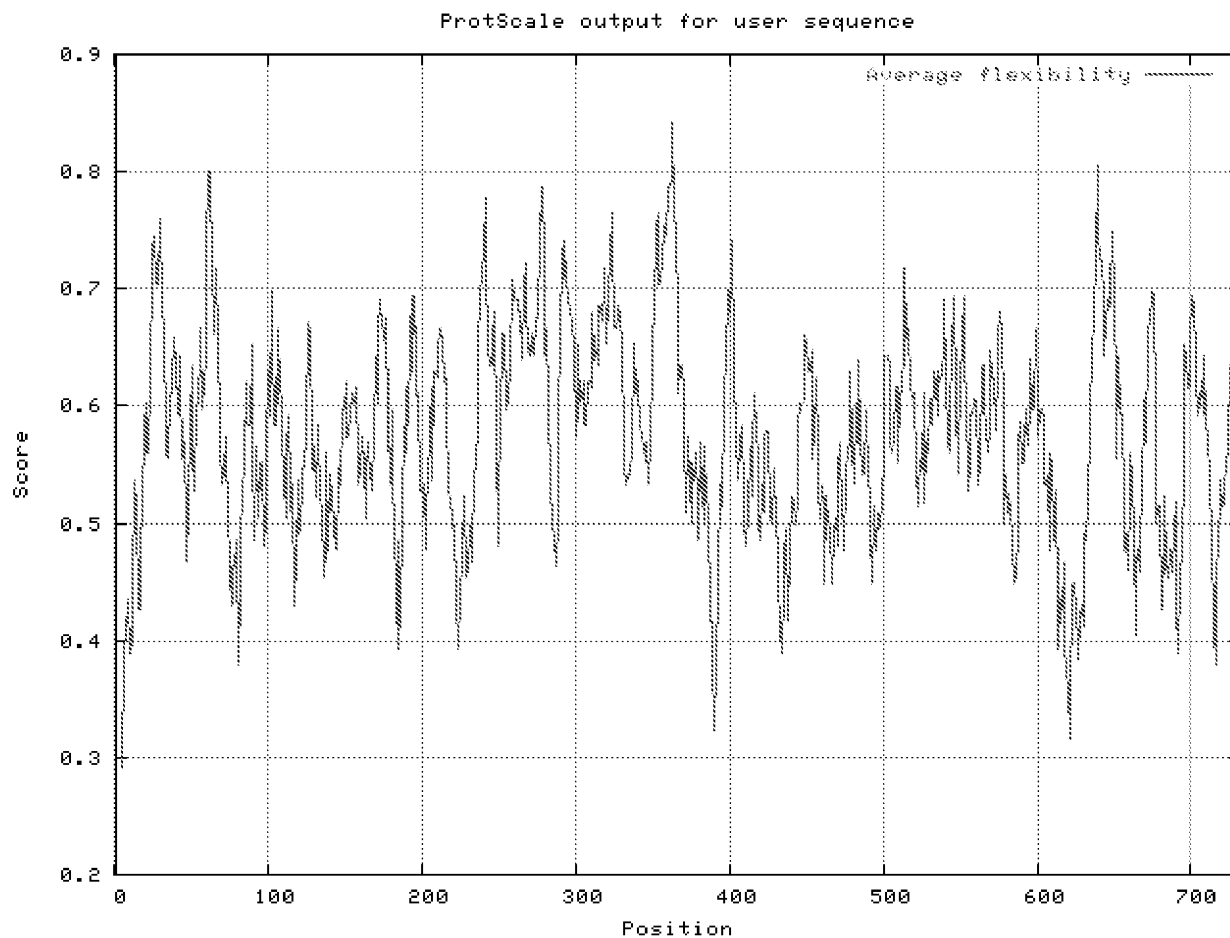


Figure 14c - 158P1D7 variant 4

Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

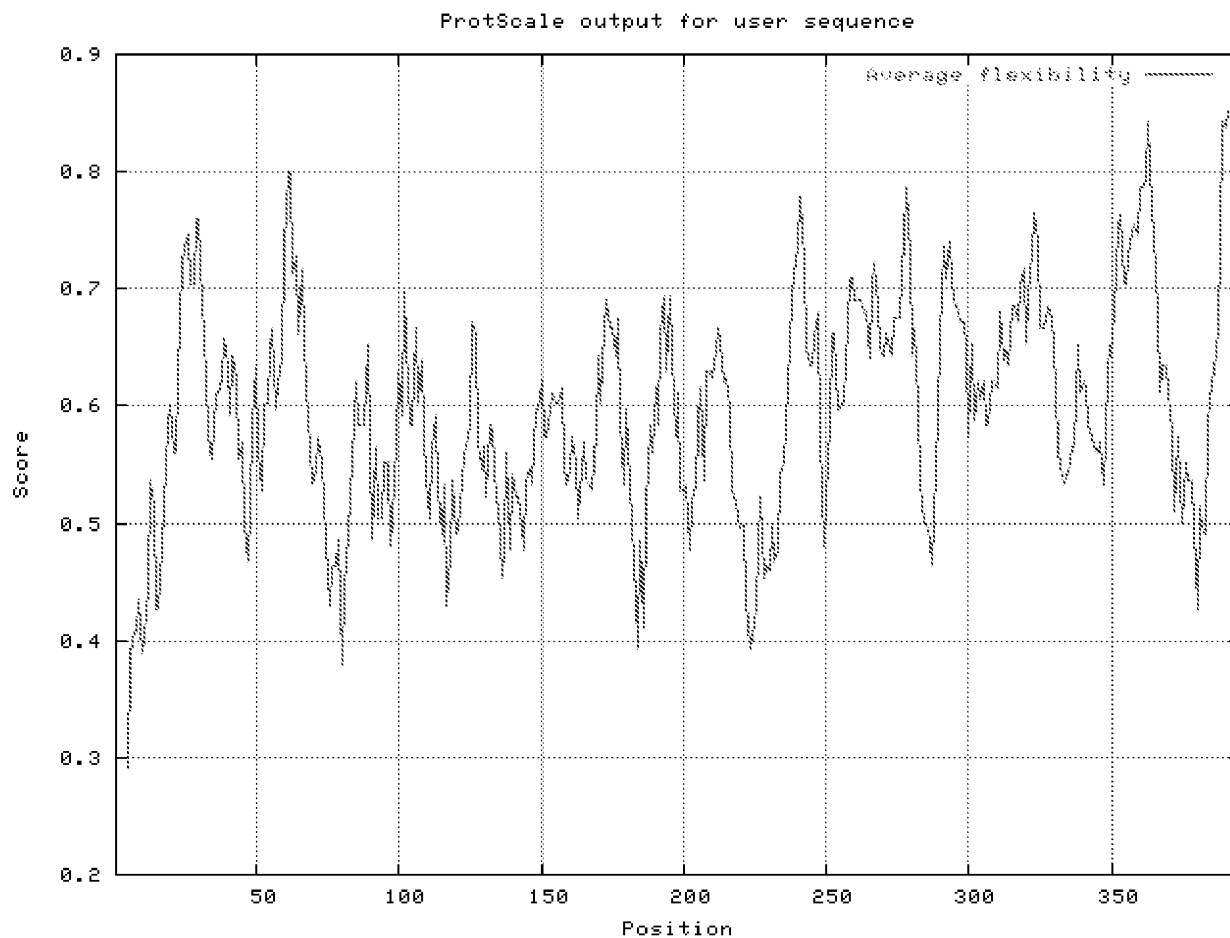


Figure 14d - 158P1D7 variant 6

Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

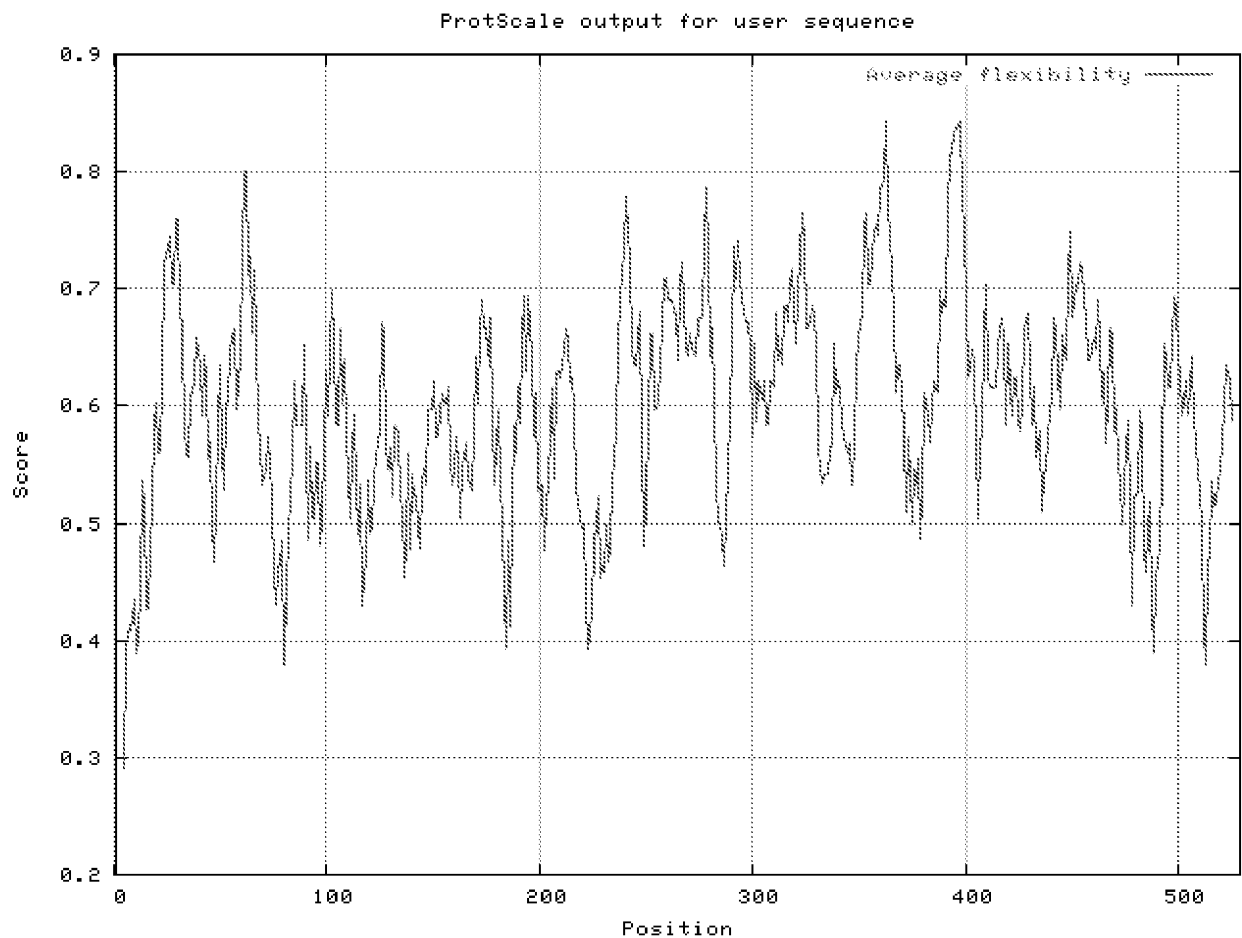


Figure 15a - 158P1D7 variant 1

Beta-turn Profile

(Deleage, G., Roux B. 1987.
Protein Engineering 1:289-294)

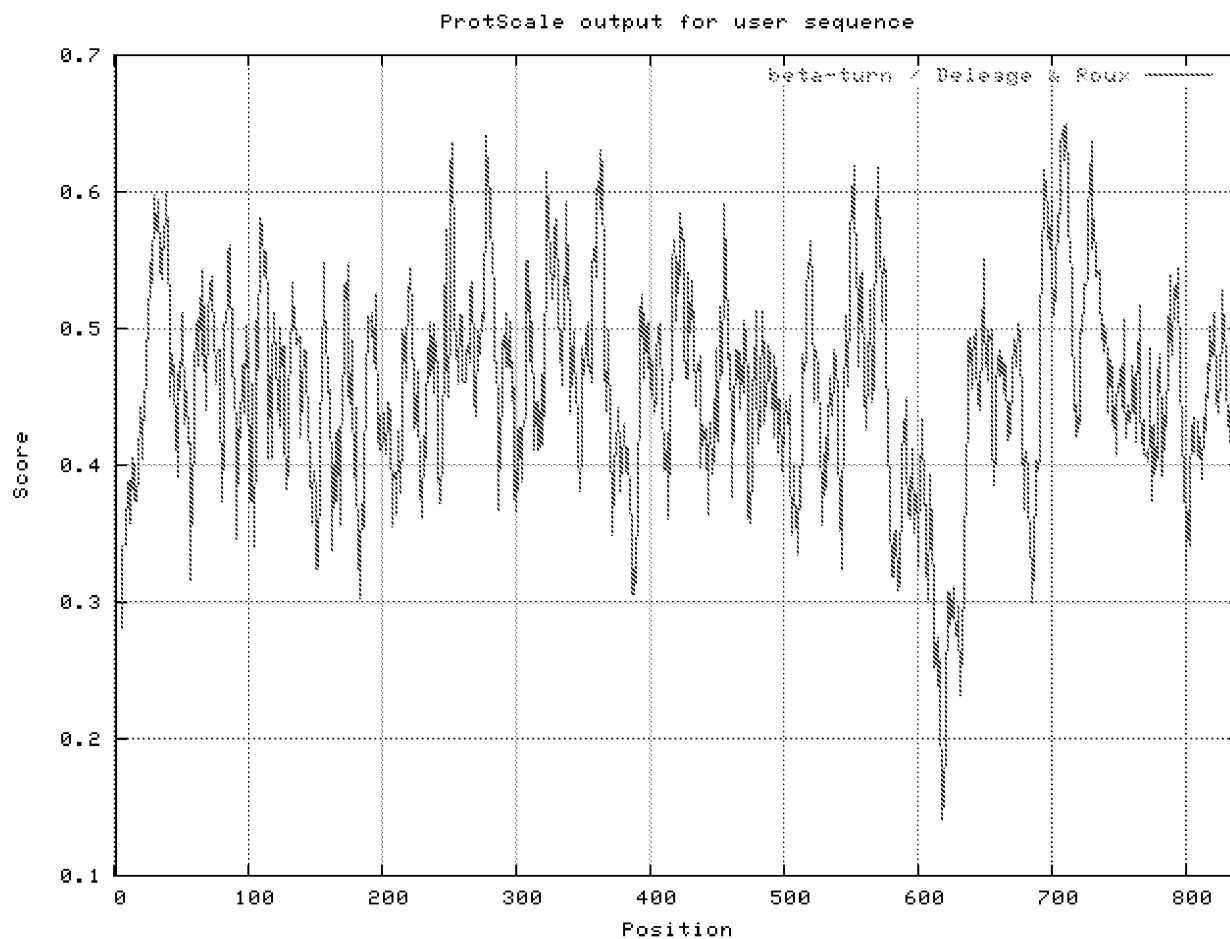


Figure 15b - 158P1D7 variant 3

Beta-turn Profile

(Deleage, G., Roux B. 1987.
Protein Engineering 1:289-294)

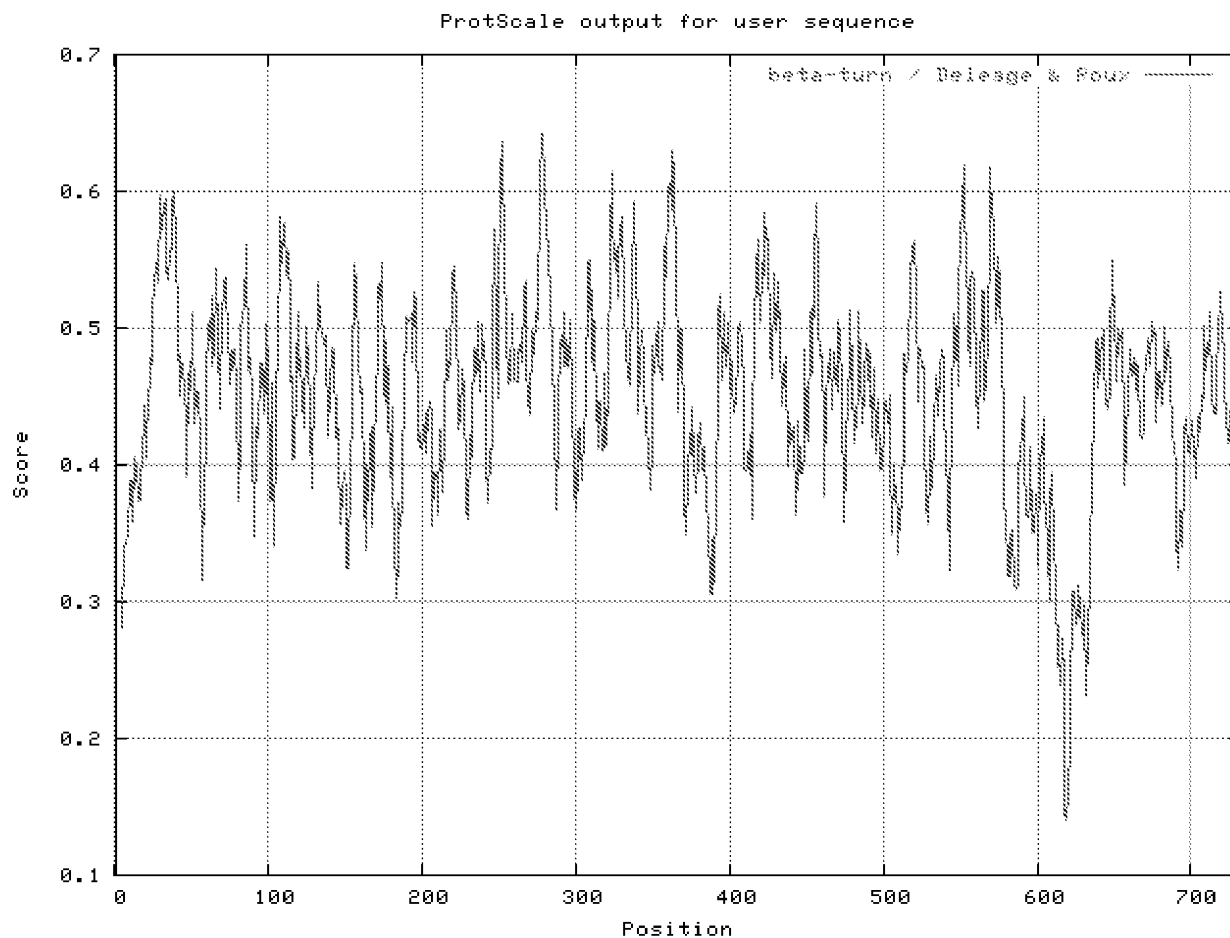


Figure 15c - 158P1D7 variant 4

Beta-turn Profile

(Deleage, G., Roux B. 1987.
Protein Engineering 1:289-294)

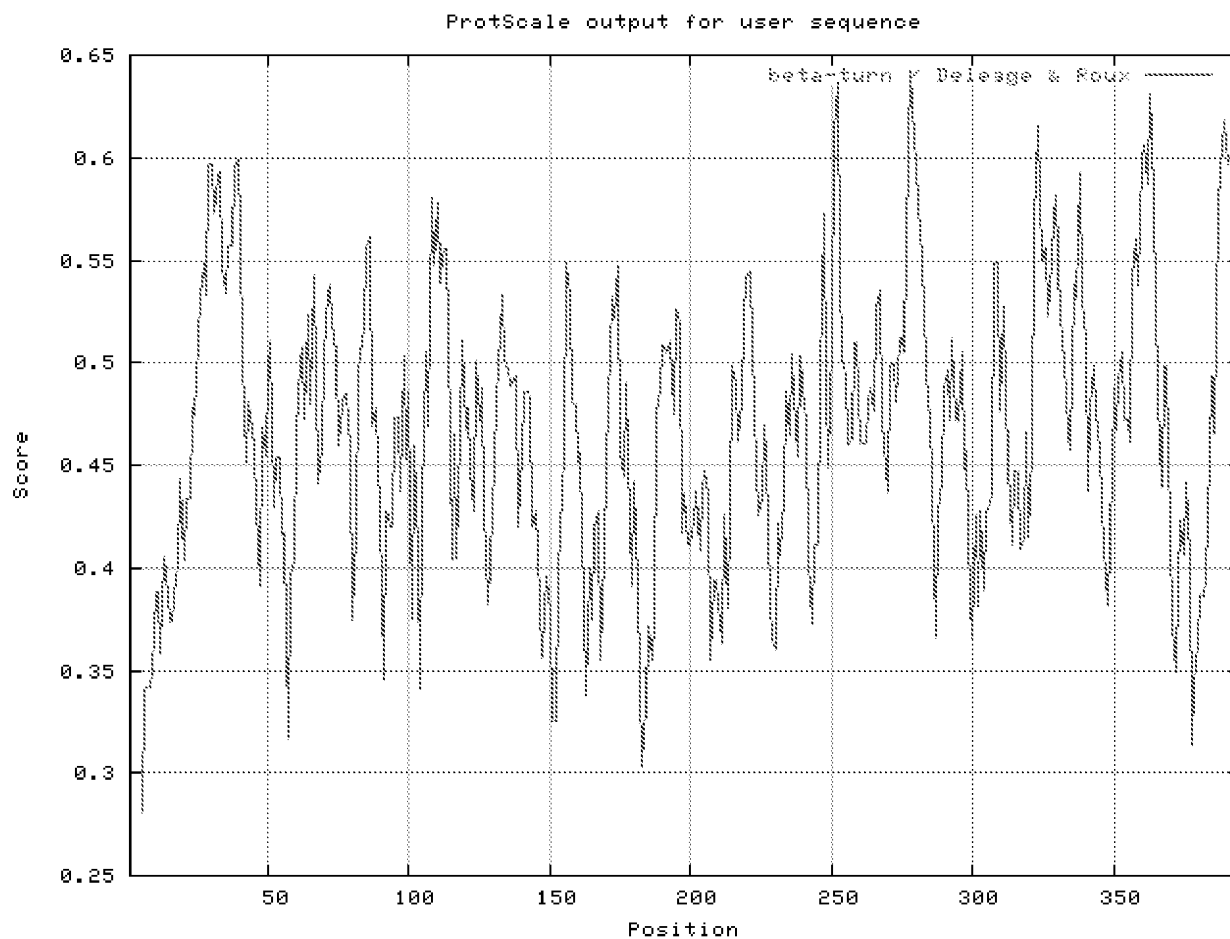


Figure 15d - 158P1D7 variant 6

Beta-turn Profile

(Deleage, G., Roux B. 1987.
Protein Engineering 1:289-294)

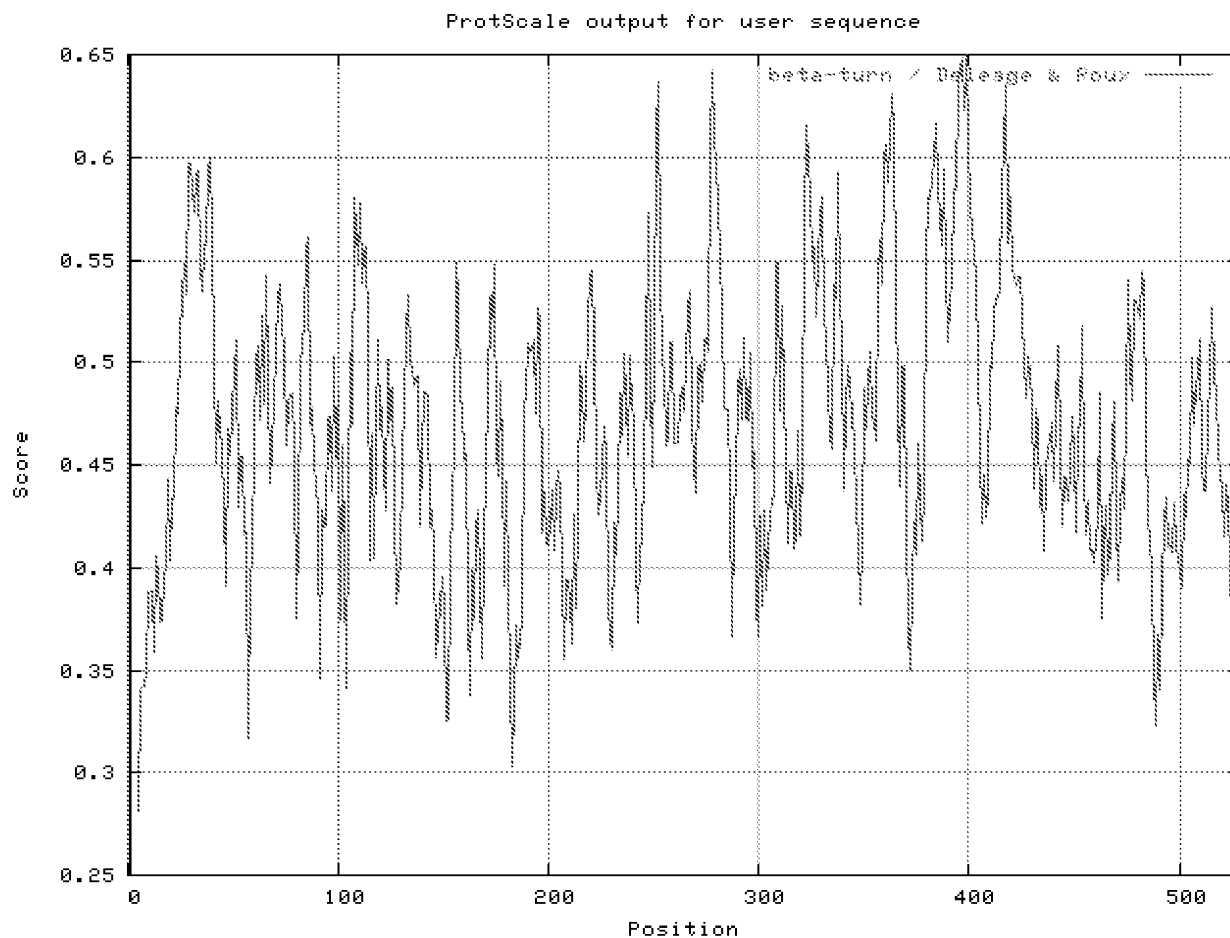
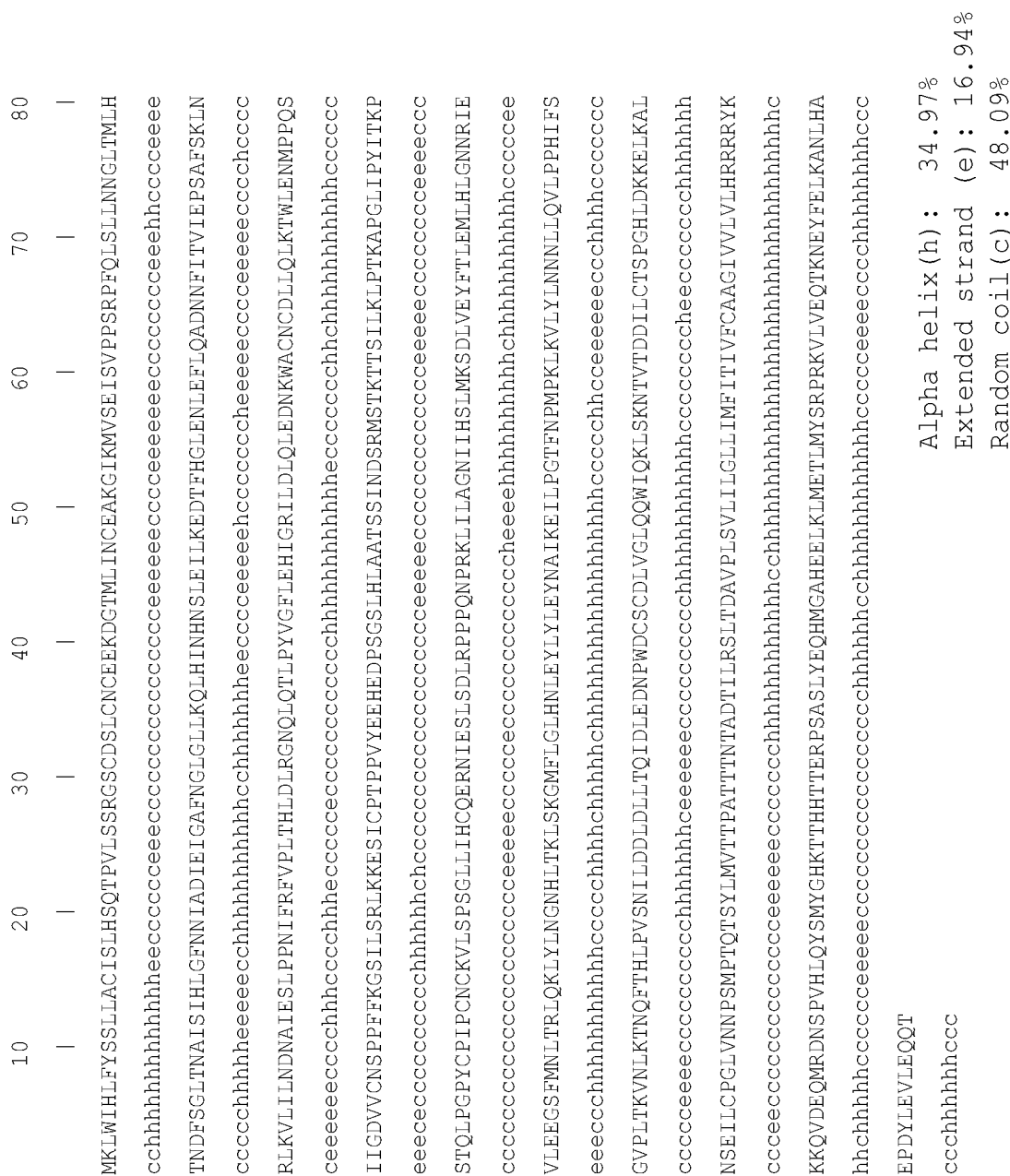
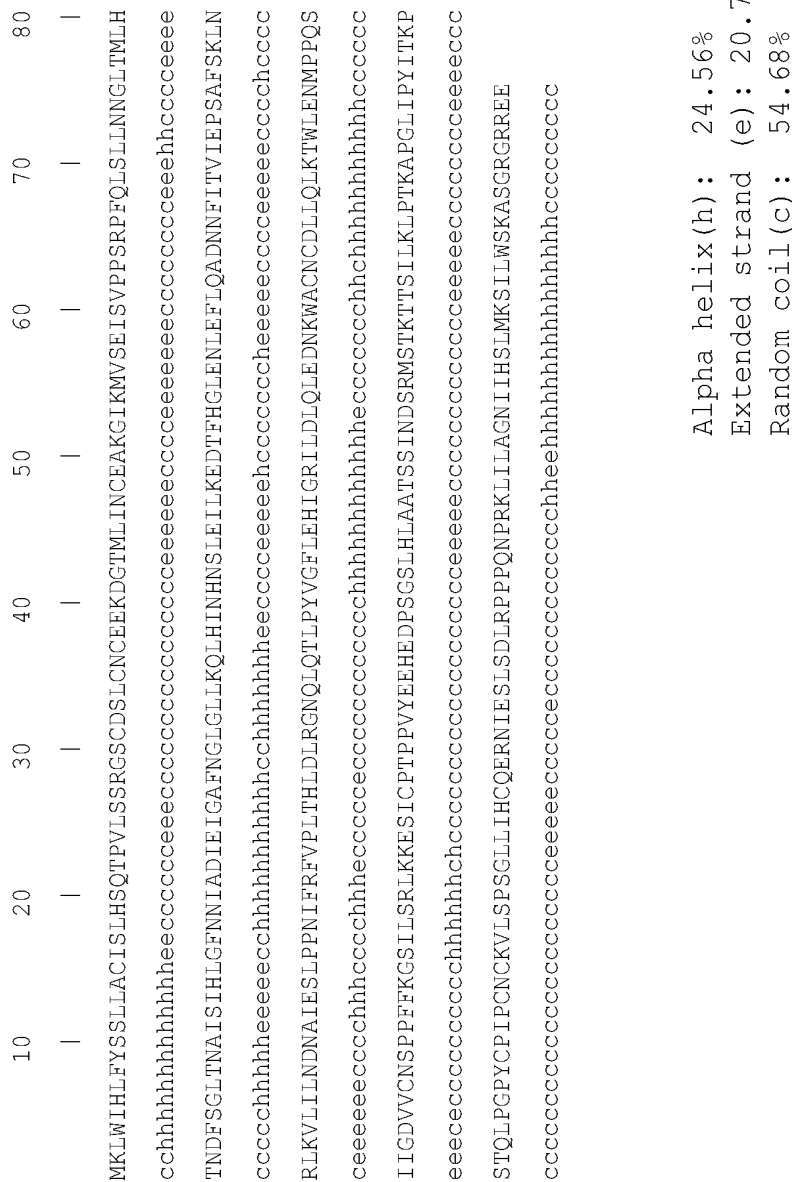


Fig 16B
Secondary structure prediction of 158P1D7 variant 3



Secondary structure prediction of 158P1D7 variant 4



Secondary structure prediction of 158P1D7 variant 6

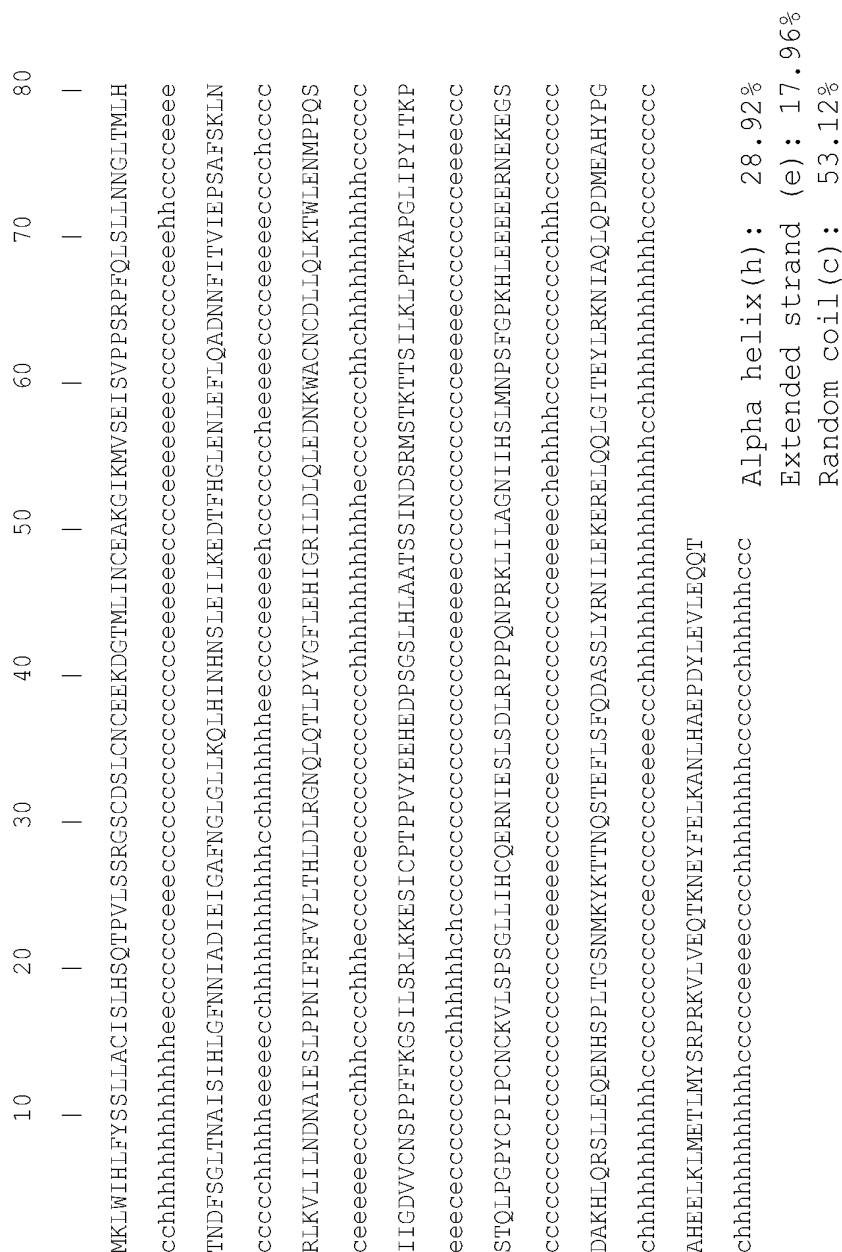
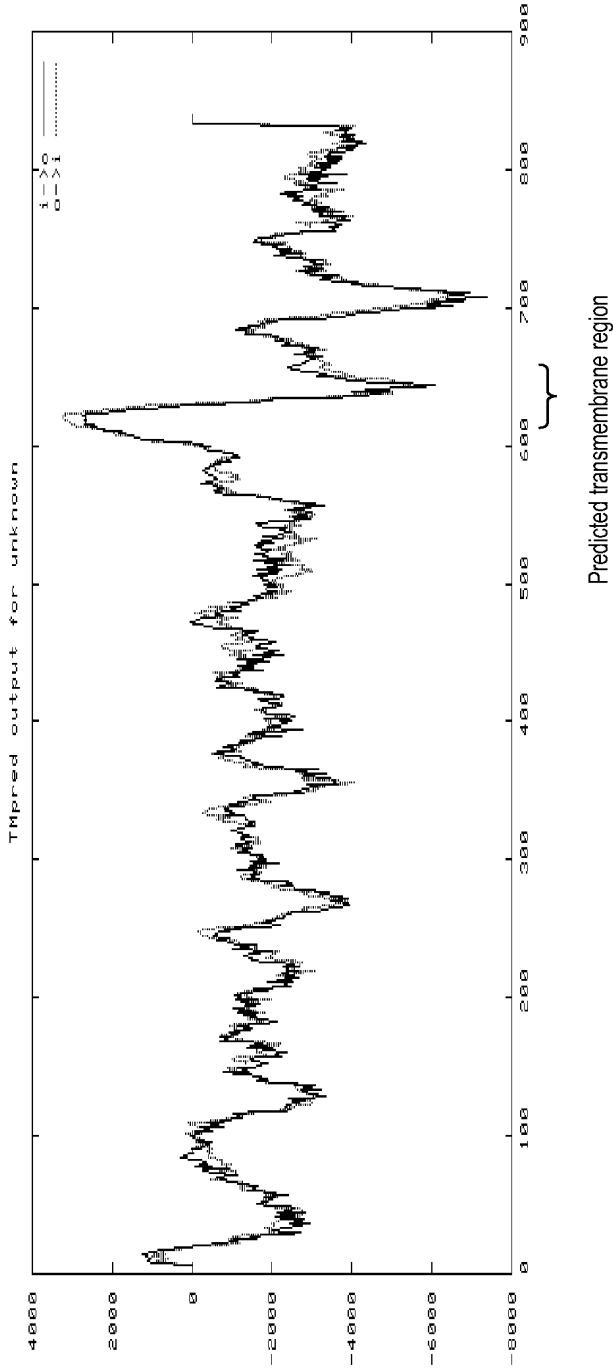


Fig 16E

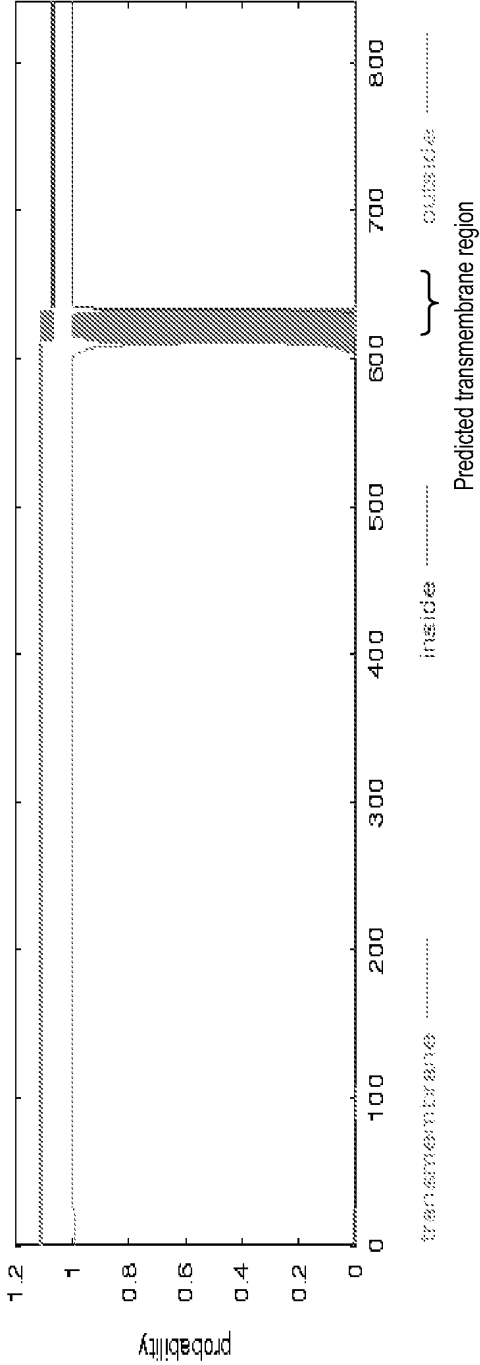
Transmembrane prediction for 158P1D7 variant 1



1 transmembrane
domain
predicted

Fig 16F

TMHMM posterior probabilities for Sequence



1 transmembrane
domain
predicted

Transmembrane prediction for 158P1D7 variant 3

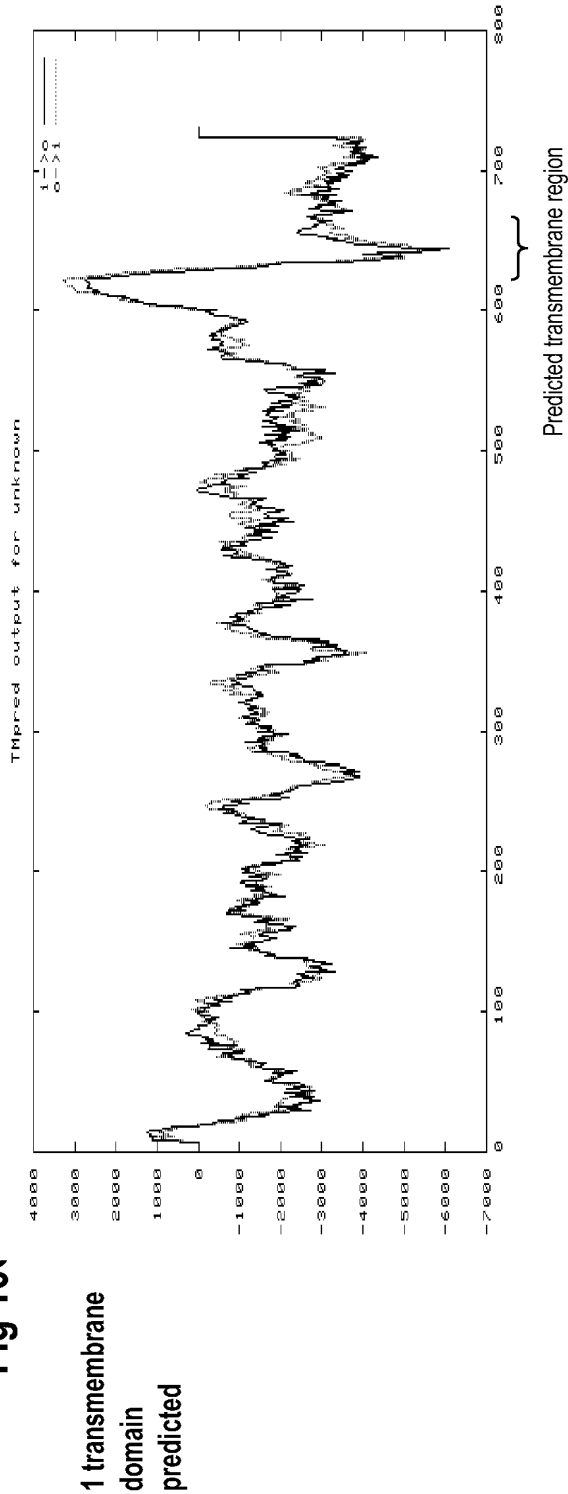


Fig 16H

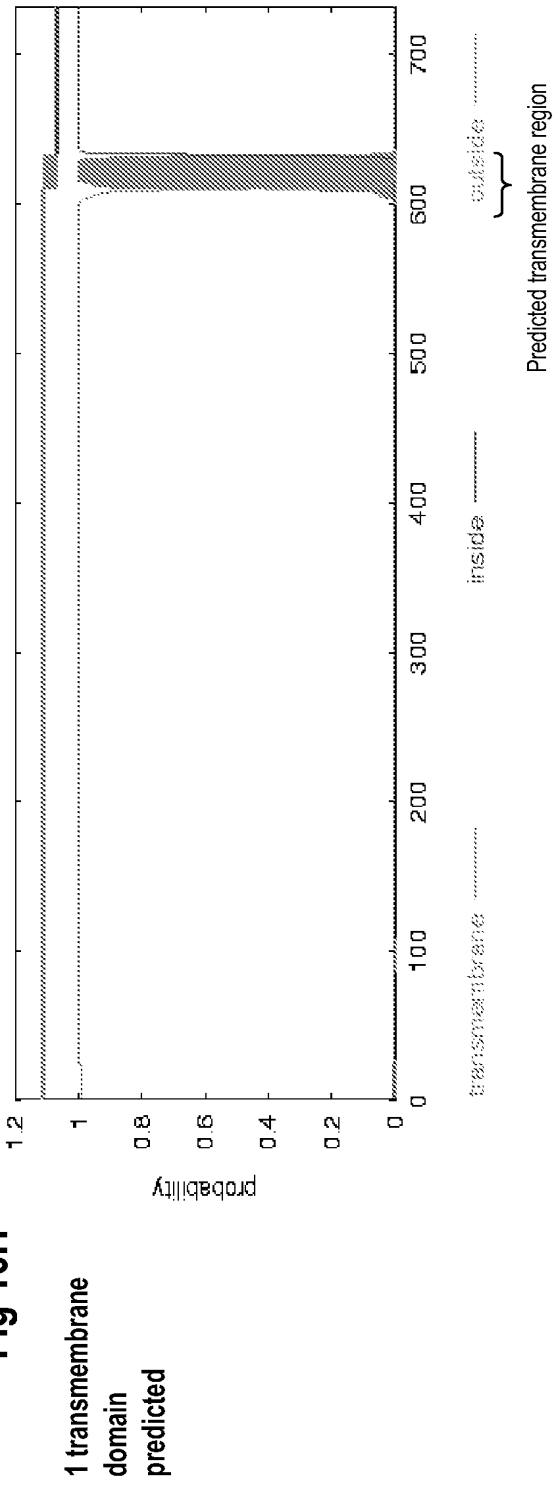
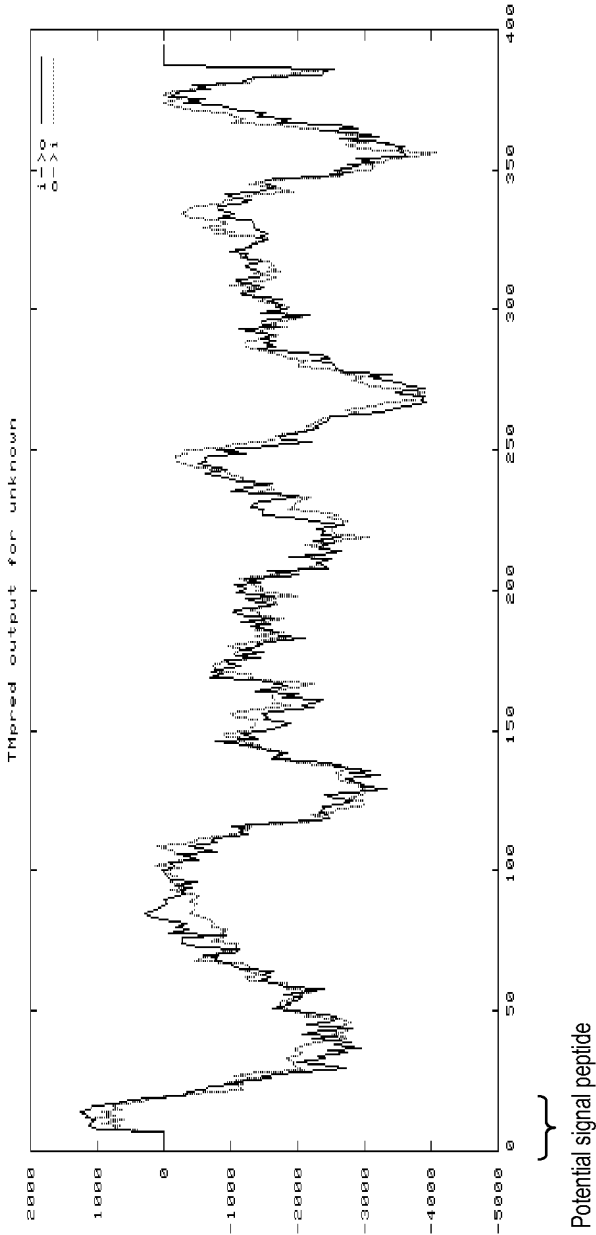


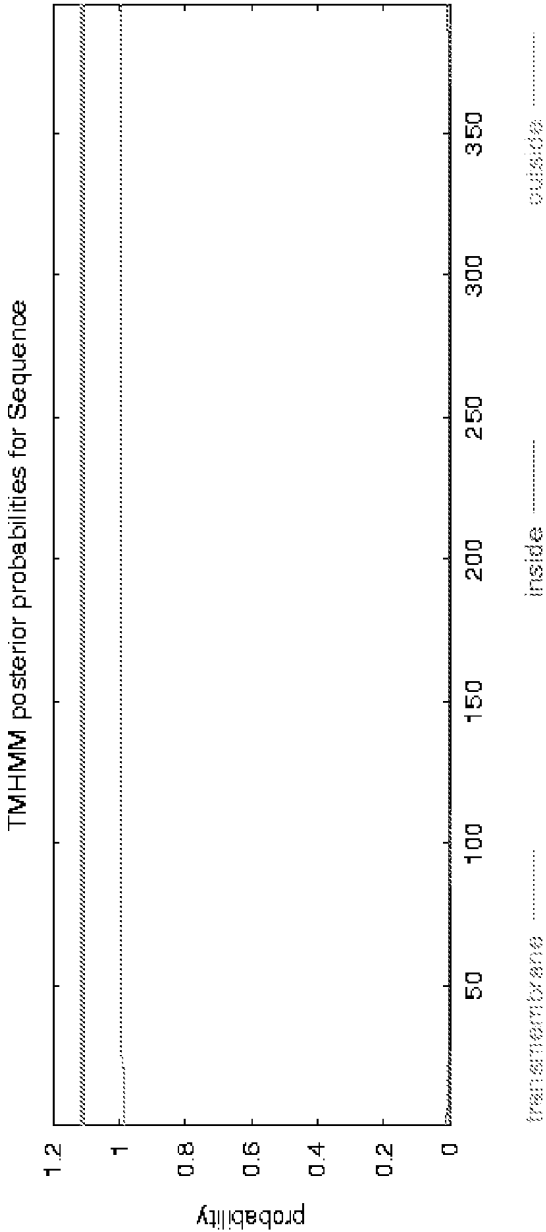
Fig 16I

Transmembrane prediction for 158P1D7 variant 4



No transmembrane
domain,
Potential signal peptide

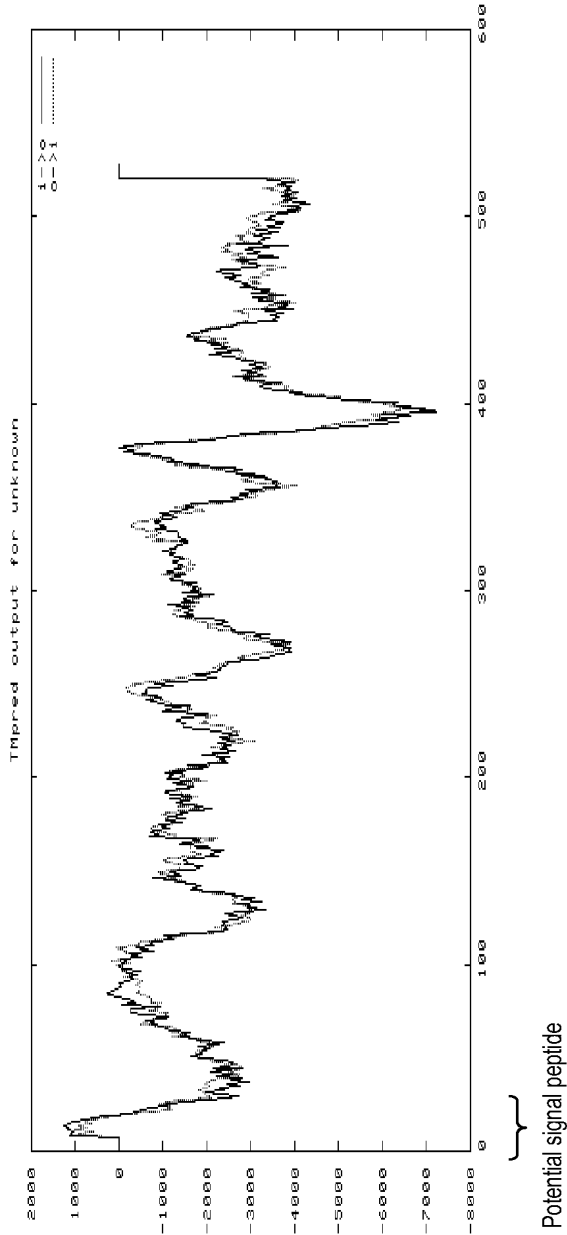
Fig 16J



No transmembrane
domain

Fig 16K

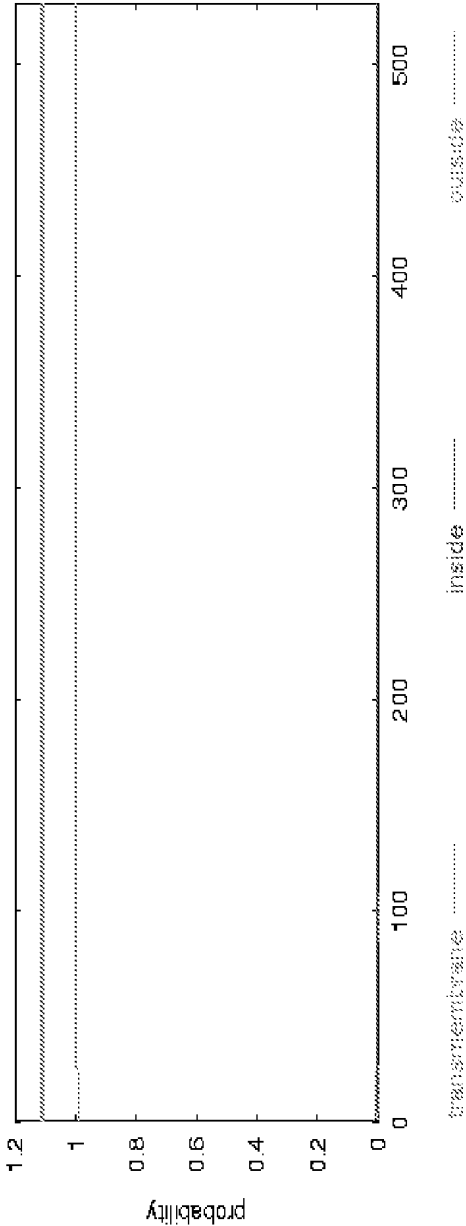
Transmembrane prediction for 158P1D7 variant 6



No transmembrane
domain,
Potential signal peptide

Fig 16L

TMHMM posterior probabilities for Sequence



No transmembrane
domain

Figure 17

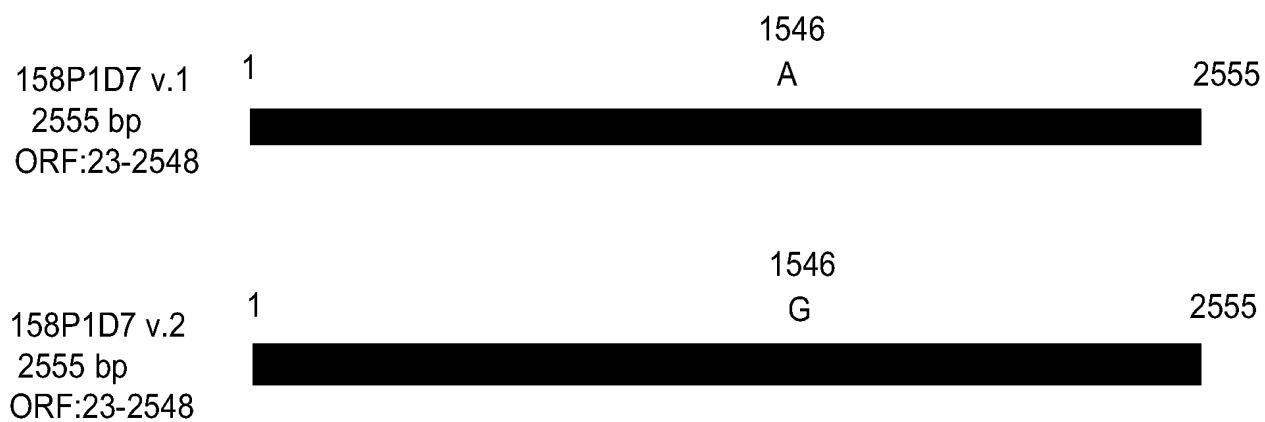


Figure 18

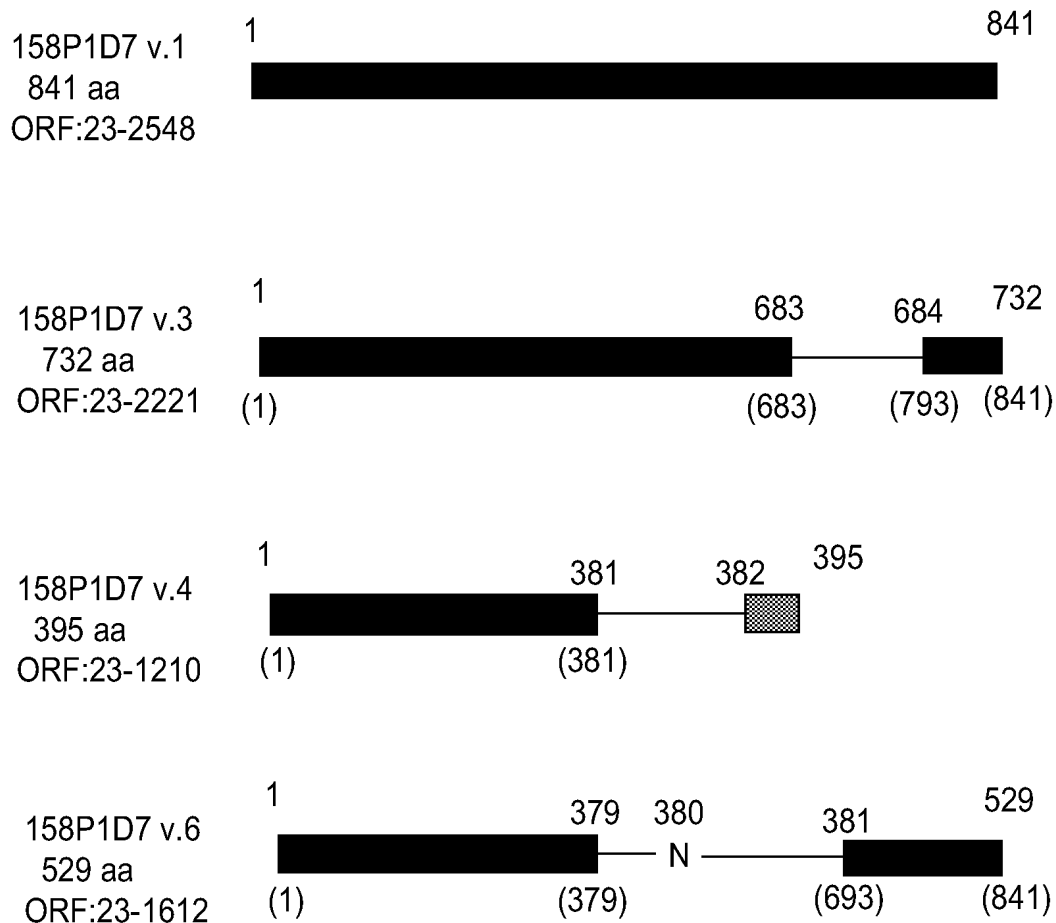


Figure 19

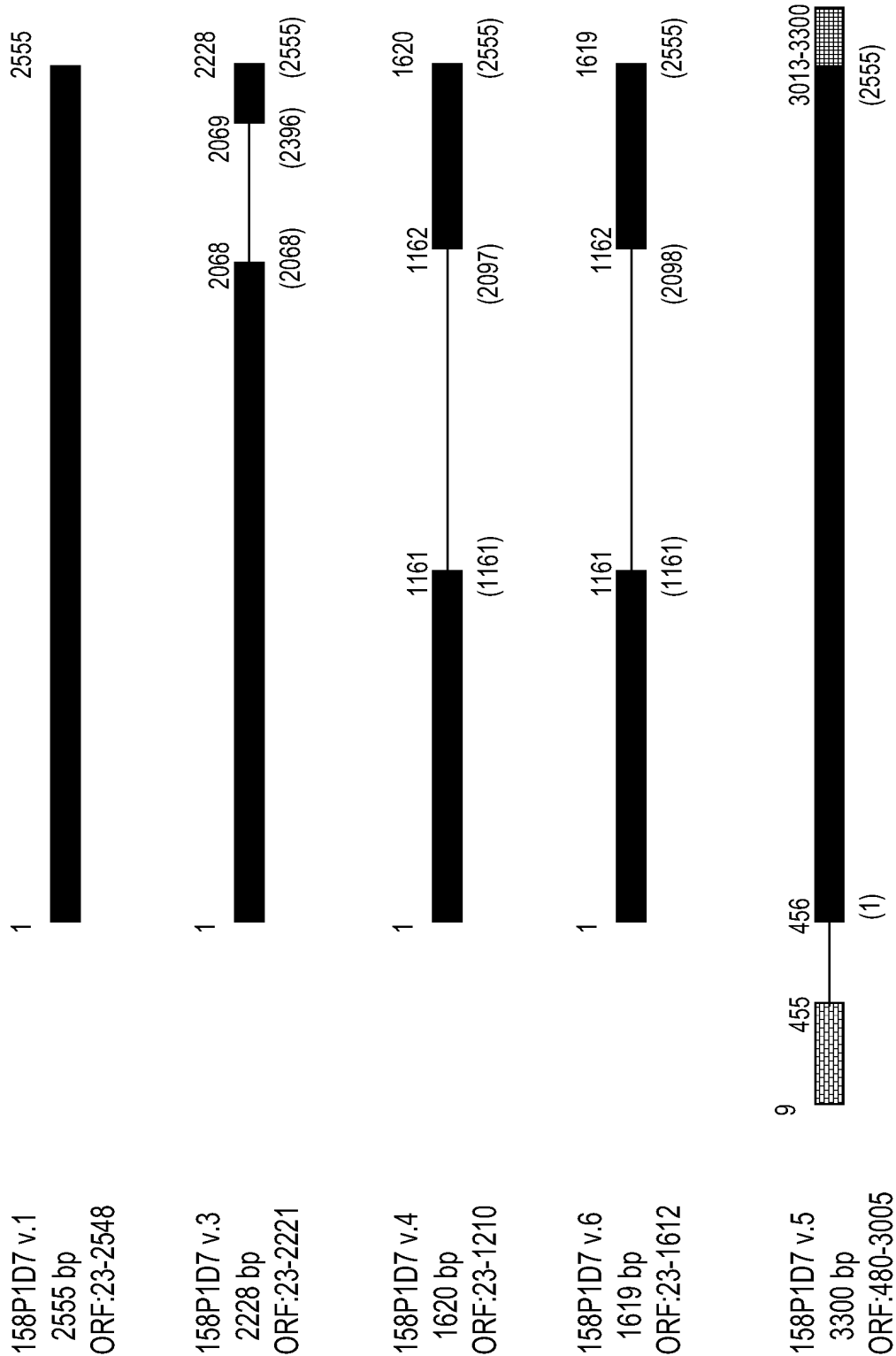
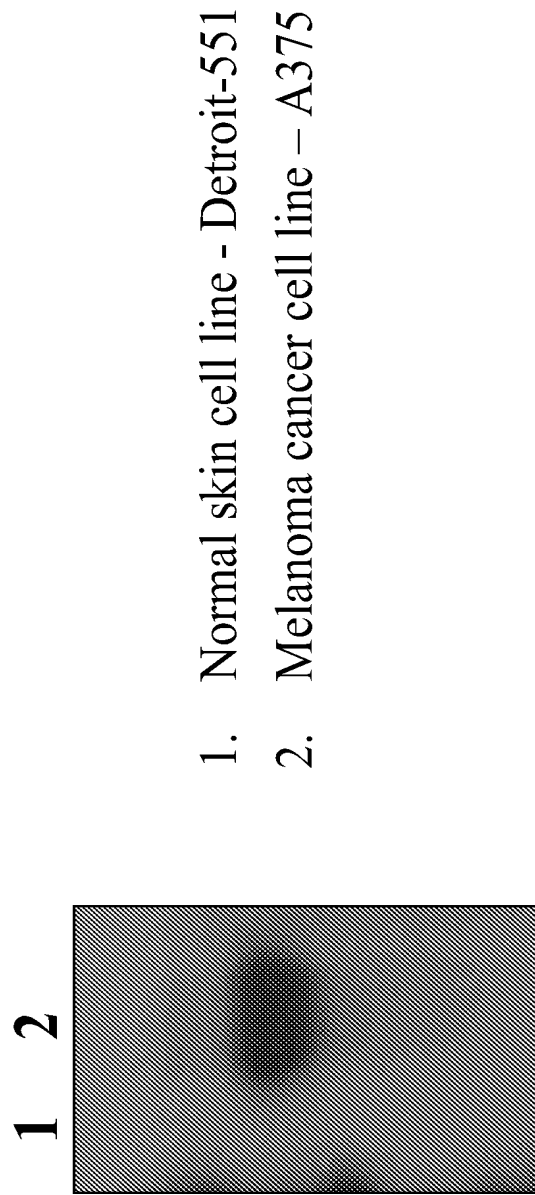


Figure 20. 158P1D7 Expression in Melanoma



**Figure 21. 158P1D7 Expression in Cervical Cancer
Patient Specimens**

Panel#	Patient ID#	Diagnosis	Grade	Stage	Cervix CA
1	Normal Cervix	(Ambion)			
2	HeLa	Cell Line			
3	USA-00281-D01	Intraepithelial neoplasia	2-3	T3AN0MX	
4	VNM-00266	AdenoCA	1	IIA	
5	VNM-00376	AdenoCA	1	IIA	
6	IND-00396	Mucinous AdenoCA	2	IIB	
7	A0098	Adenosquamous	2B	T2bNXM0	

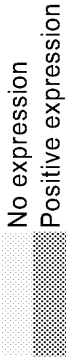


Figure 22: Detection of AGS15 protein in recombinant cells with monoclonal antibodies

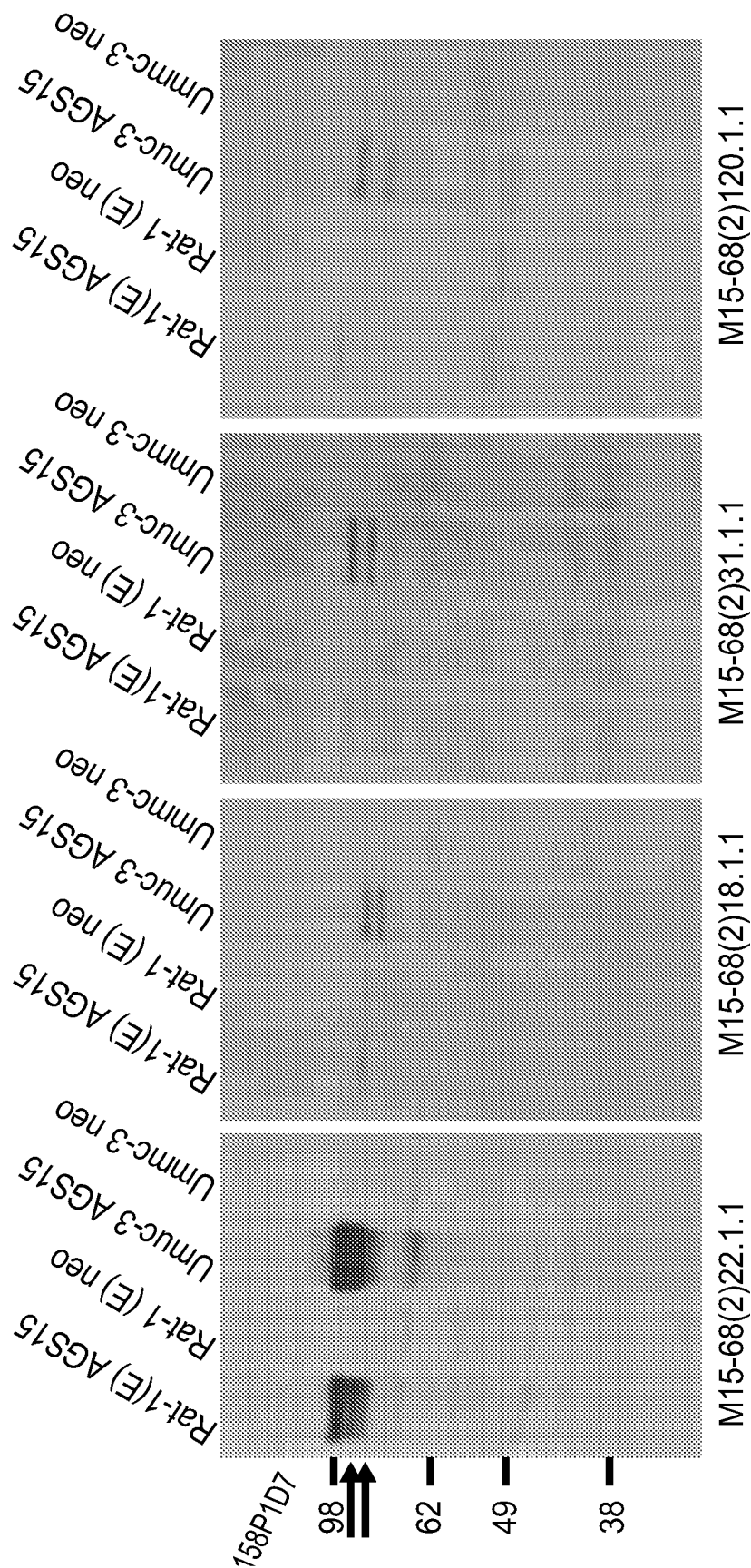


Figure 23: Surface staining of AGS15-expressing 293T and UMUC cells with anti-AGS15 monoclonal antibodies

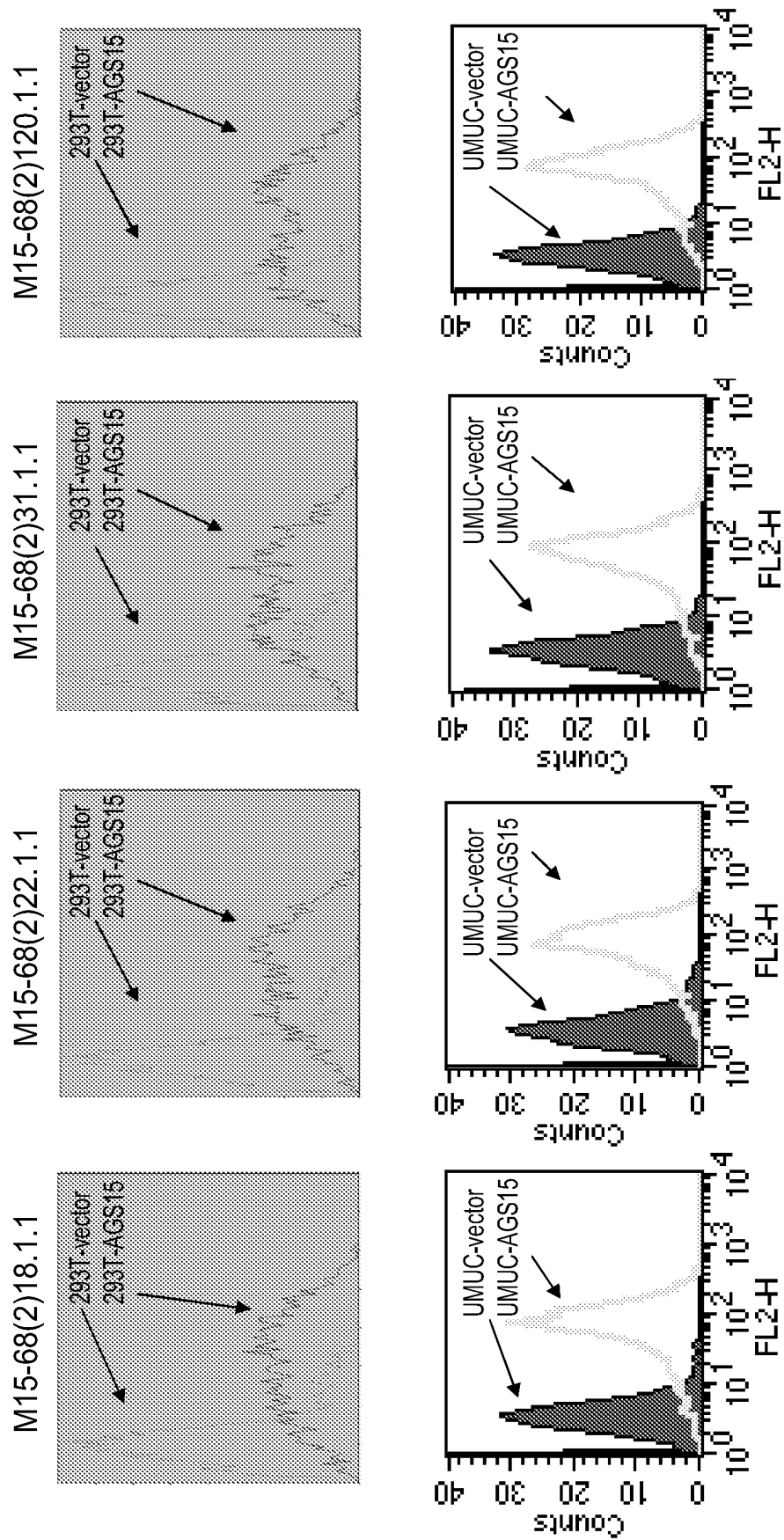


Figure 24: Surface staining of endogenous AGS15-expressing LAPC9 prostate cancer and UGB1 bladder cancer xenograft cells with MAb M15-68(2)22.1.1

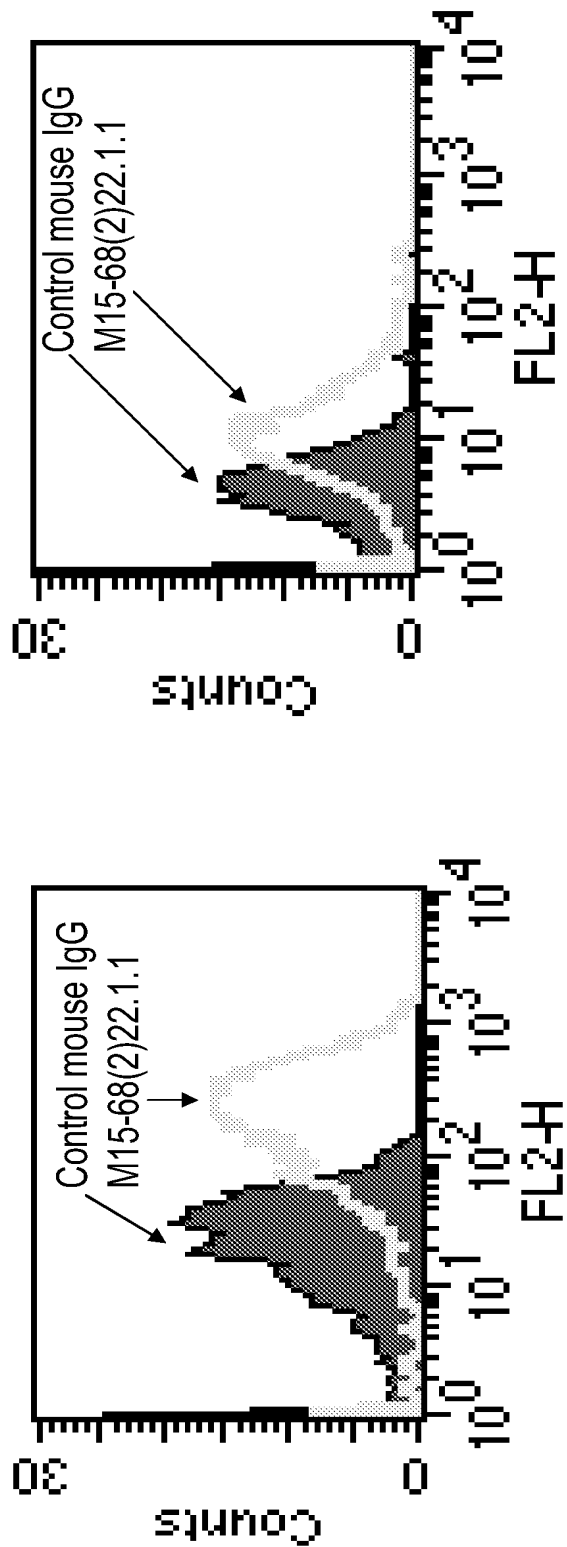


Figure 25-1: Monoclonal antibody-mediated internalization of endogenous surface 158P1D7 in NCI-H146 small cell lung cancer cells

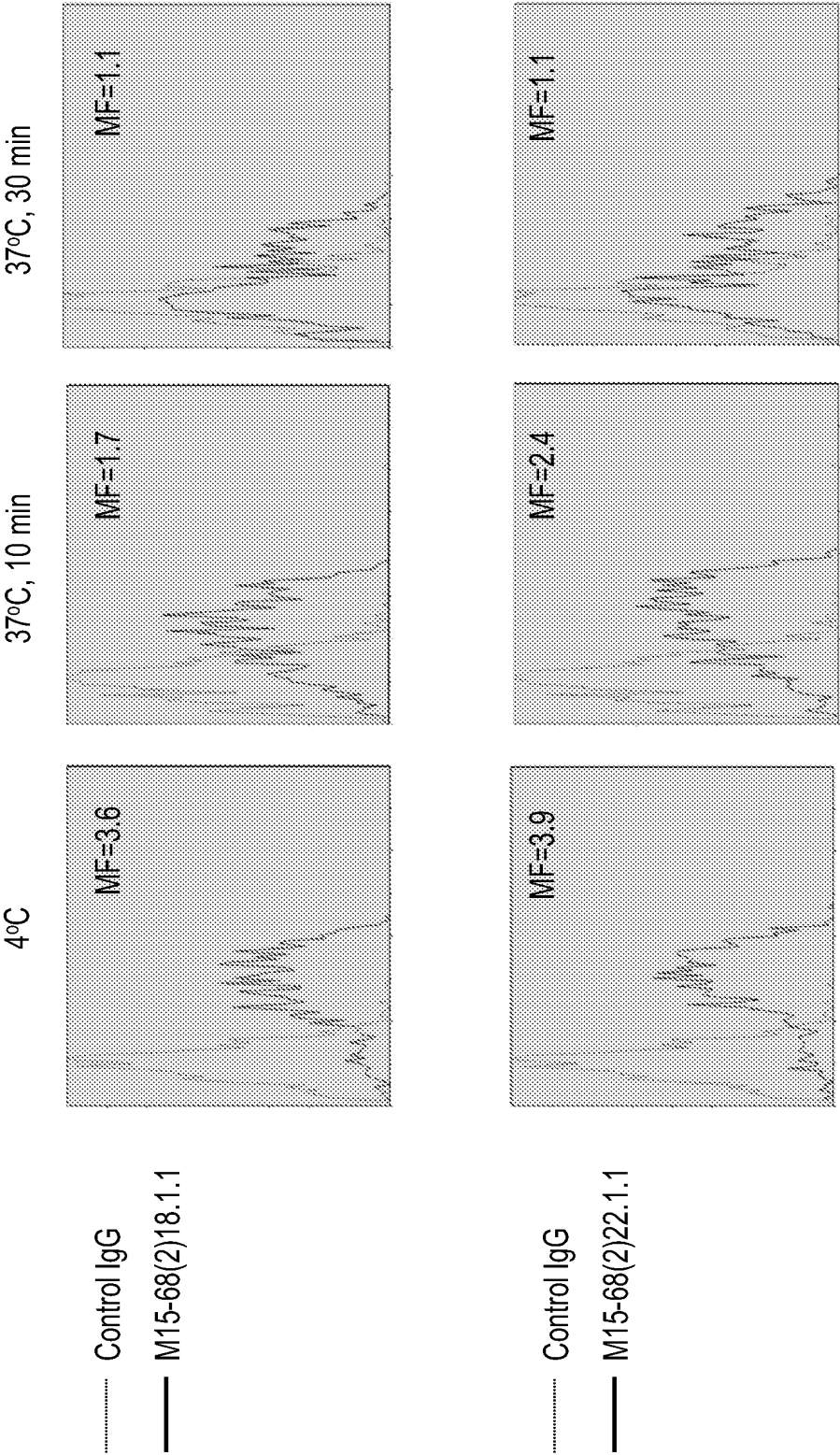


Figure 25-2

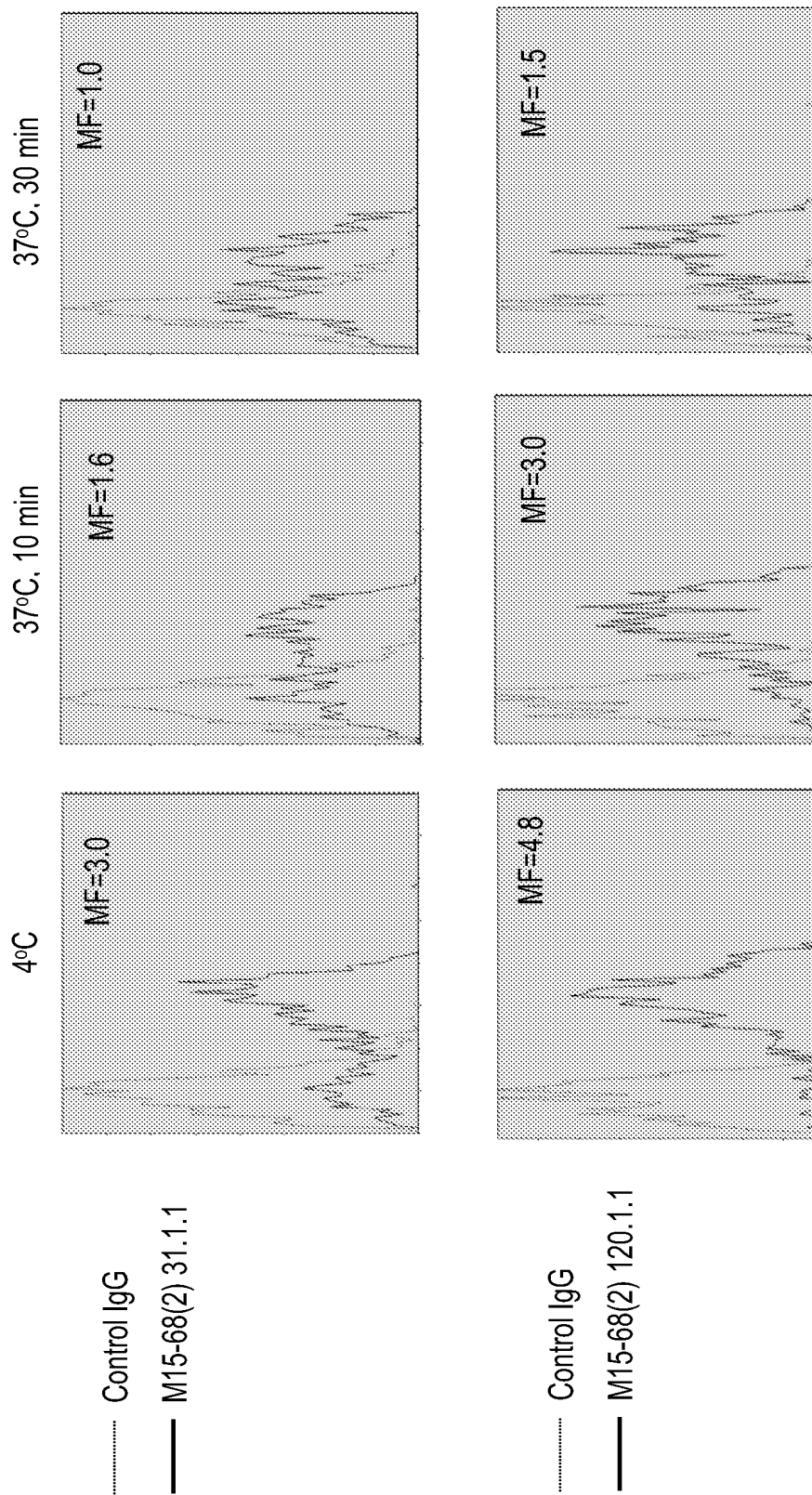


Figure 26: Binding of the 158P1D7 extracellular domain to human umbilical vein endothelial cells (HUVEC)

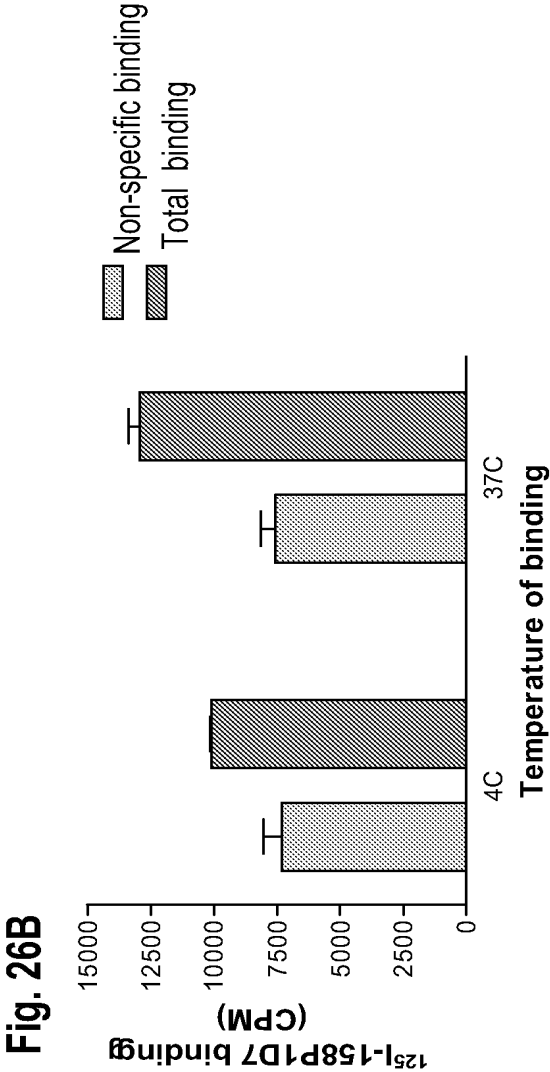
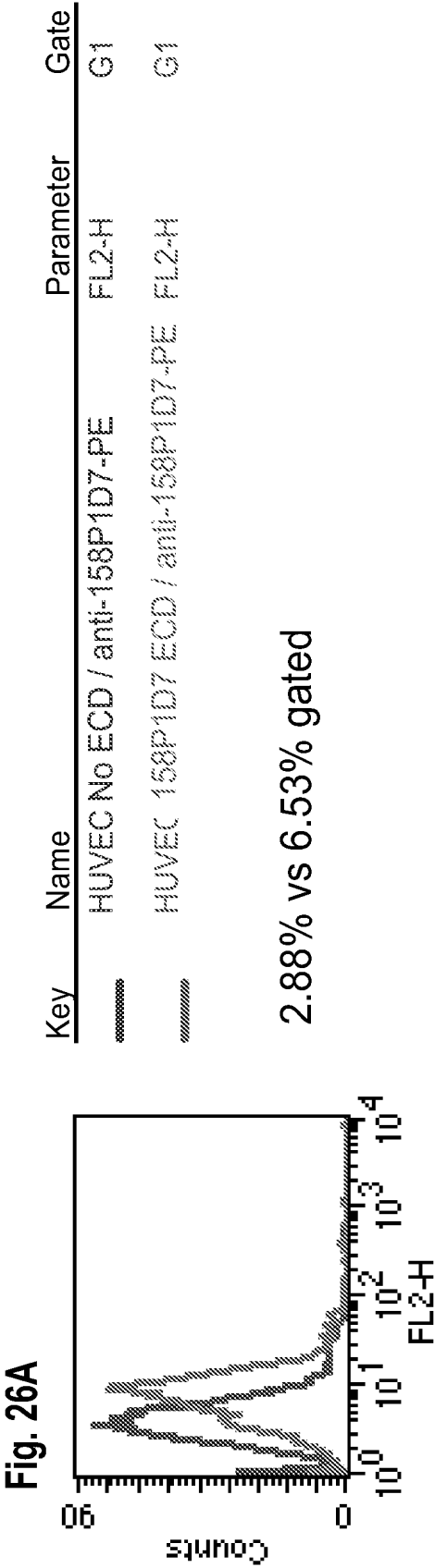


Figure 27 - 158P1D7 Enhances the Growth of Bladder Cancer UM-UC-3 Cells in Mice

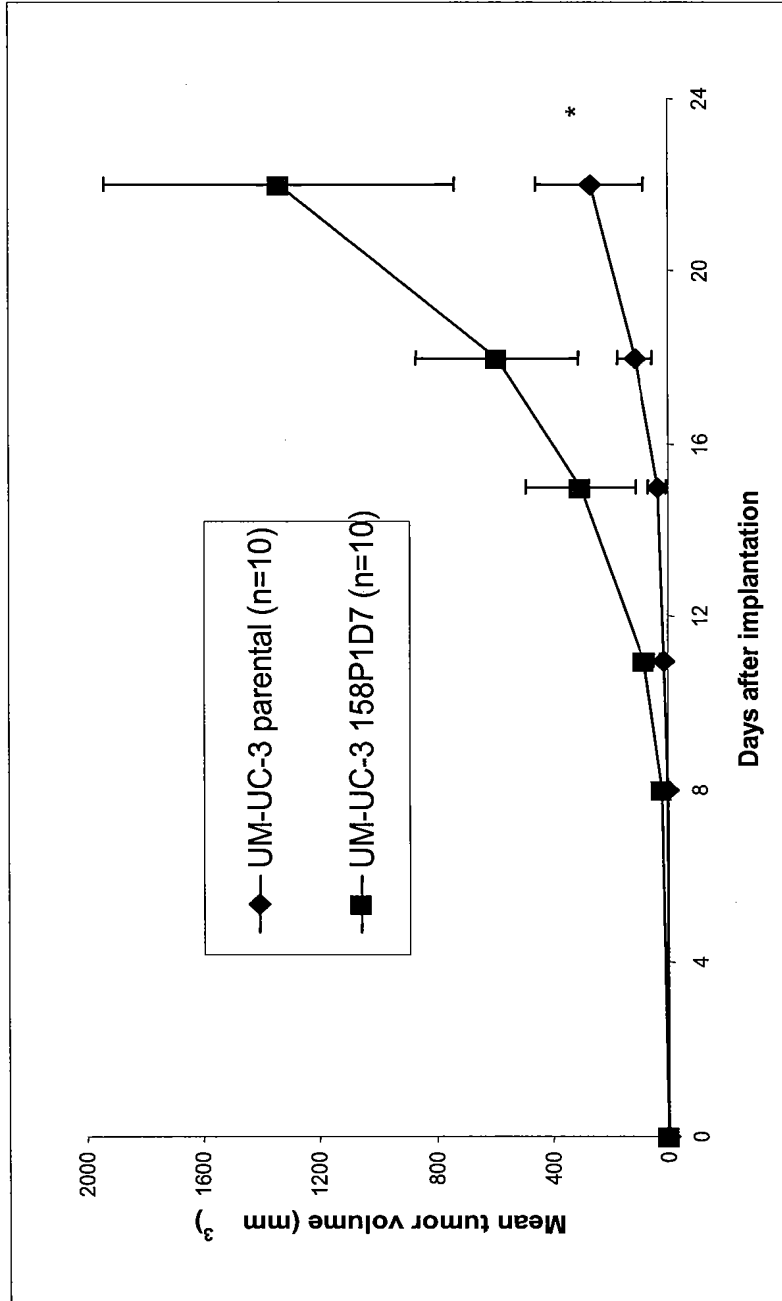
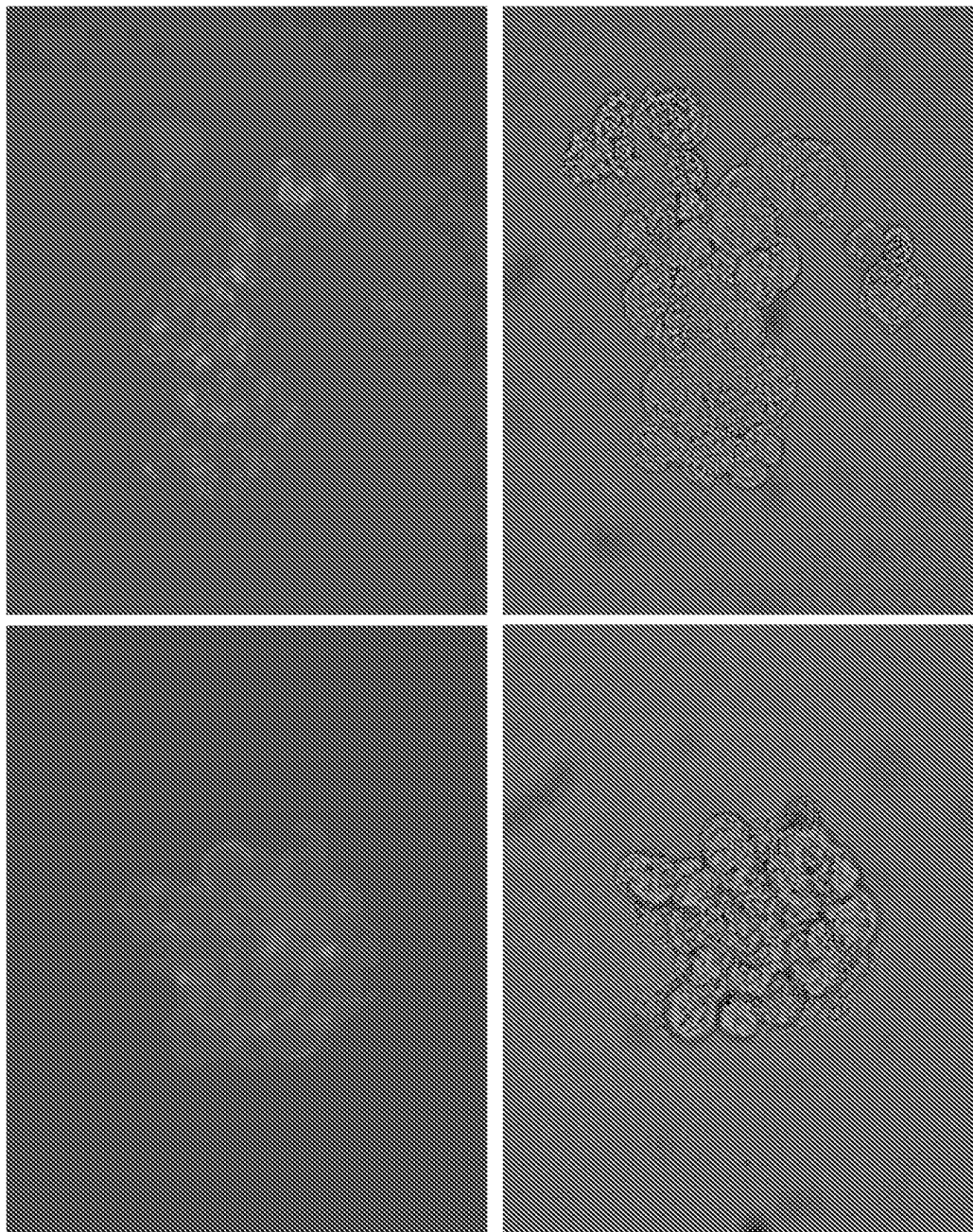


Figure 28: Internalization of MAb M15-68(2).31.1.1 in NCI-H146 cells
4C → 37C for 30 min



Fluorescence

Bright Field

Figure 29: Effect of 158P1D7 RNAi on cell survival

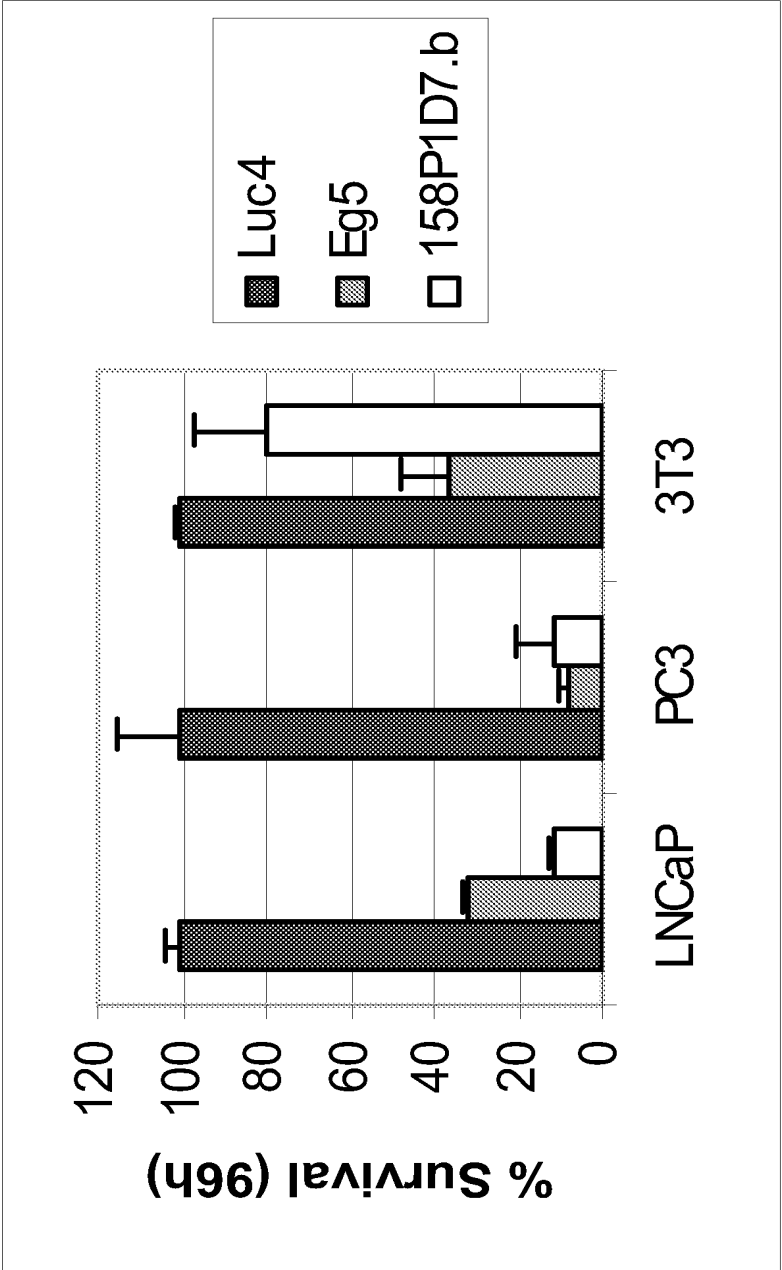


Figure 30 - 158P1D7 MAbs Retard the Growth of Human Bladder Cancer Xenografts in Mice

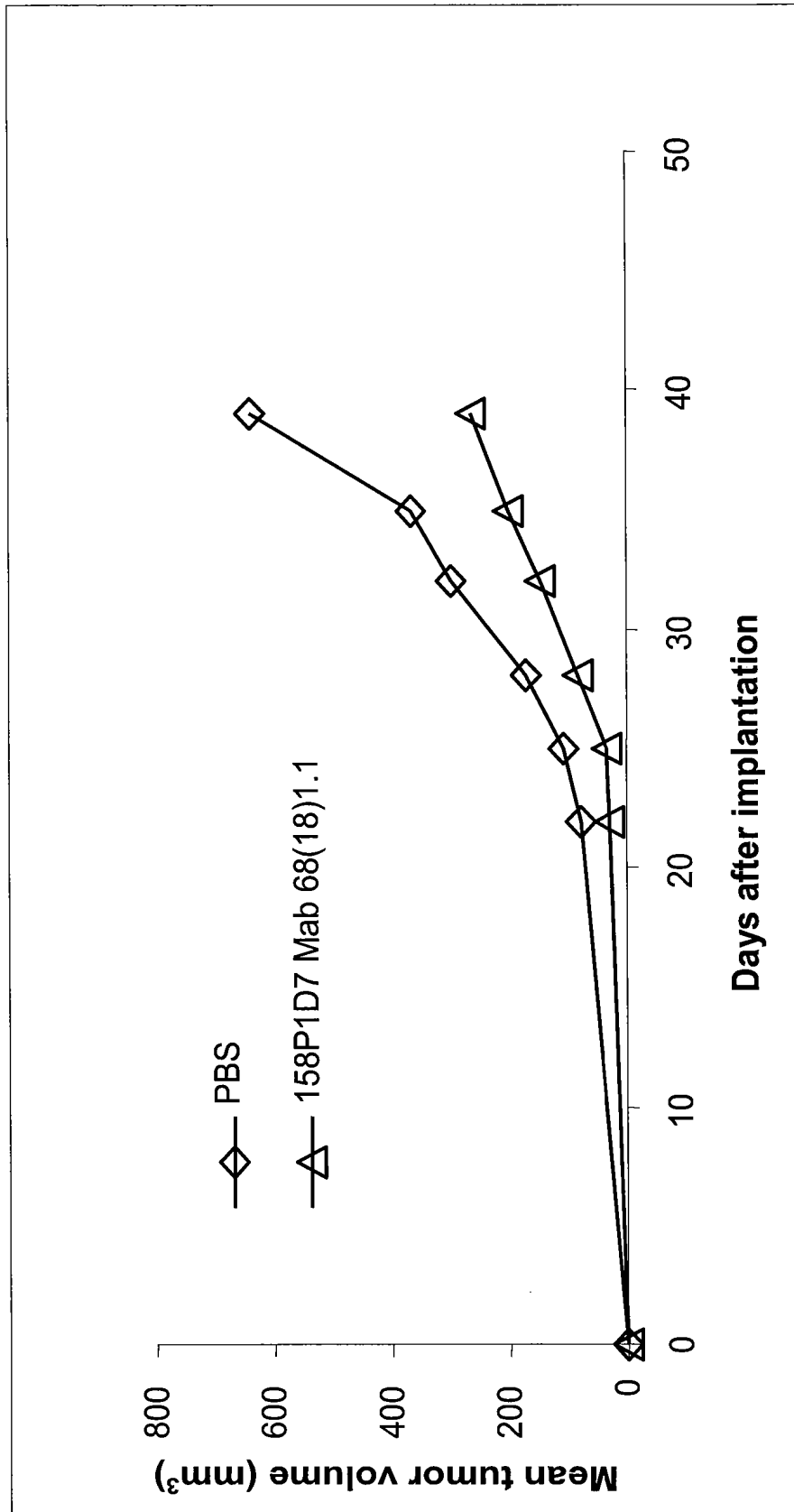


Figure 31 - 158P1D7 MAbs Retard Growth of Human Prostate Cancer Xenografts in Mice

Patient-derived LAPC9 xenograft

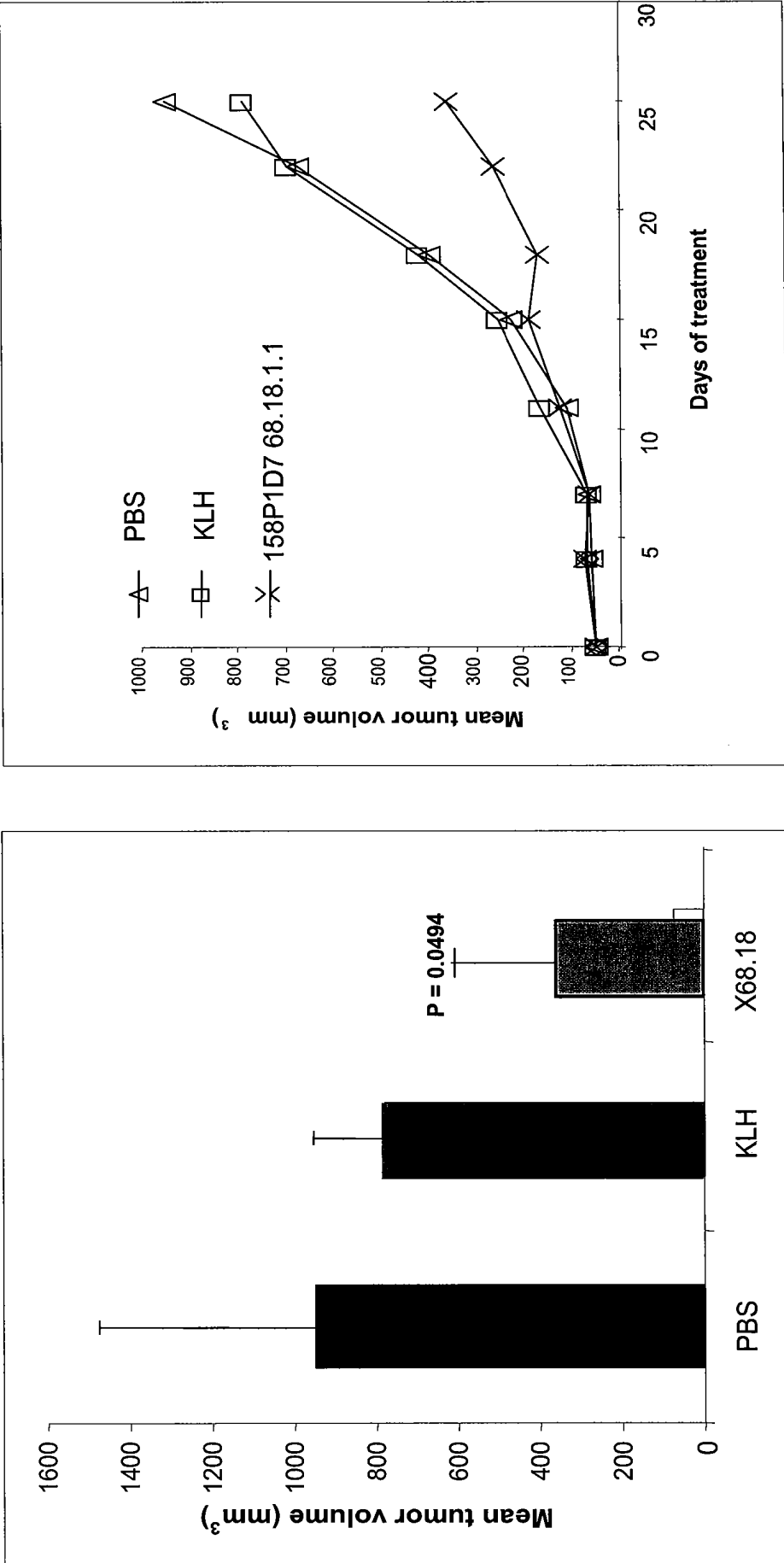


Figure 32: Effect of 158P1D7 on Proliferation of Rat1 cells

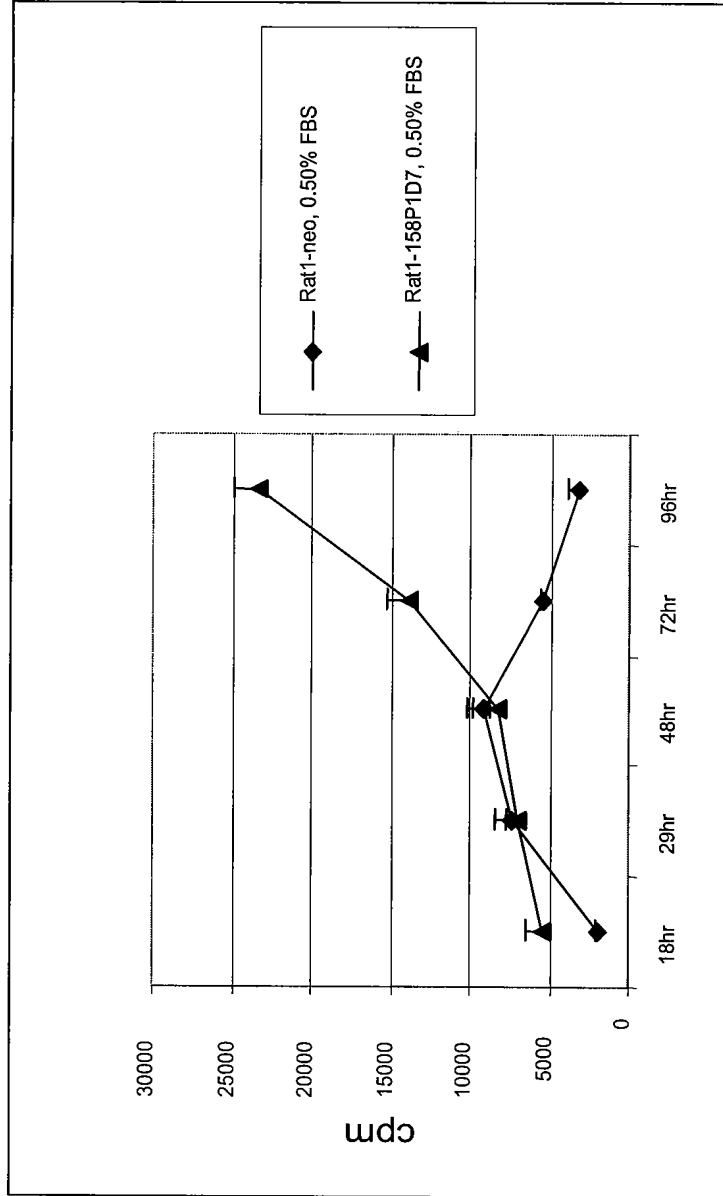


Figure 33: 158P1D7 Enhances Entry Into the S Phase

Cells	Treatment	Percent Cells		
		G1	S	G2
3T3	0.5% FBS	92.7	2.6	2.2
	10% FBS	72.8	11.4	14.7
3T3-neo	0.5% FBS	95.1	1.4	2.3
	10% FBS	59.6	14.1	18.3
3T3-158P1D7	0.5% FBS	90.1	3.3	4.4
	10% FBS	68.4	21.2	1.7

Figure 34A. The cDNA and amino acid sequence of M15/X68(2)18 VH clone #1.

```
1 Q T A G V R S W P G G A L T E P V H H M
1 1 caaactgcaggagtcaggagttggcctggtggcgccctcacagagcctgtccatcacatg
21 H R L R I L I D R L W C K L G S P A S R
61 caccgtctcaggattctcattgacccggtatggtgtaaaactgggttcgccagcctccagg
41 K G S G V A G N D L G R W K H R L Y F S
121 aaagggtctgggggtggctgggaatgatttggggcgatggaagcacagattatacttcagc
61 S P I Q T E H Q E G Q F K S Q T F L K N
181 tctccaatccagactgagcatcaggaaggacaattcaagagccaaactttcttaaaaaat
81 N S L Q T D D T A R Y Y C A R D E G R G
241 aacagtctgcaaactgatgacacagccaggtattactgtgccagagatgaagggagggga
101 L C L I A G A K G P R S P S P
301 ctctgtttgattgctggggccaagggaccacggtcacctctcctca
```

Figure 34B. The cDNA and amino acid sequence of M15/X68(2)18 VL clone #2.

```
1 D I Q L T Q S P A S L A V S L G Q R A T
1 1 gacattcagctgacccagtcctcctgcttccttagctgtatctcttggggcagagggccacc
21 I S Y R A S K S V S T S G Y S Y M H W N
61 atctcatacagggccagcaaaagtgtcagtagatcttggtatagttatatgcactggaac
41 Q Q K P G Q P P R L L I Y L V S N L E S
121 caacagaaaccaggacagccacccagactcctcatctatcttgtatccaacctagaatct
61 G V P A R F S G S G S G T D F T L N I H
181 ggggtccctgccaggttcagtggcagtggtctgggacagacttcaccctcaacatccat
81 P V E E E D A A T Y Y C Q H I R E L T R
241 cctgtggaggaggaggatgctgcaacctattactgtcagcacattagggagcttacacgt
101 S E G G P S W R S N
301 tcggaggggggaccaagctggagatctaac
```


Figure 35A: The amino acid sequence of M15/X68(2)18 VH clone #1.

```
1  QTAGVRSWPG  GALTEPVHHM  HRLRILIDRL  WCKLGSPASR  KGSGVAGNDL
51  GRWKHRLYFS  SPIQTEHQEG  QFKSQTF LKN  NSLQTDDTAR  YYCARDEGRG
101 LCLIAGAKGP  RSPSP
```

Figure 35B: The amino acid sequence of M15/X68(2)18 VL clone #2.

```
1  DIQLTQSPAS  LAVSLGQRAT  ISYRASKSVS  TSGYSYMHWN  QQKPGQPPRL
51  LIYLVSNLES  GVPARFSGSG  SGTDFTLNIH  PVEEEDAATY  YCQHIRELTR
101 SEGGPSWRSN
```

**Figure 36: Detection of 158P1D7 protein by immunohistochemistry
in various cancer patient specimens**

